

GenCore version 5.1.6
Copyright (c) 1993 - 2003 .Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:17:47 ; Search time 53.3338 Seconds
(without alignments)
1348.171 Million cell updates/sec

Title: US-09-802-077-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2432	100.0	453	14 AAR33311	Humanised MaEl1 Ve
2	2432	100.0	453	21 AAY85199	Heavy chain amino
3	2391	98.3	451	20 AAW95659	Mus musculus anti-
4	2391	98.3	451	20 AAW95661	Mus musculus anti-
5	2391	98.3	451	21 AAY85201	Light chain amino
6	2391	98.3	451	22 AAB47088	Anti-IgE antibody,
7	2391	98.3	451	22 AAB76948	Full length heavy
8	2391	98.3	451	22 AAB76950	Full length heavy
9	2369	97.4	451	20 AAY50031	Human E27 anti-IgE

10	2369	97.4	451	20 AAW95663	Mus musculus anti-
11	2369	97.4	451	21 AAB07473	Amino acid sequenc
12	2369	97.4	451	22 AAB74212	E27 anti-IgE antib
13	2369	97.4	451	22 AAB76952	Full length heavy
14	2214.5	91.1	452	20 AAY29458	Recombinant immuno
15	2214.5	91.1	452	21 AAB30322	Humanised anti-IL-
16	2214.5	91.1	452	21 AAY77766	Humanised anti-IL-
17	2214.5	91.1	452	24 ABU59512	Humanised Mouse an
18	2214.5	91.1	452	24 ABU13799	Humanised mouse an
19	2210	90.9	476	23 ABB81110	Anti-VEGF heavy ch
20	2207.5	90.8	447	24 AAE33522	Human AQC2 heavy c
21	2205.5	90.7	452	19 AAW69316	Anti-IL-8 humanise
22	2204.5	90.6	477	22 AAU14288	Human novel protei
23	2201.5	90.5	447	24 AAE33523	Human AQC2 heavy c
24	2197.5	90.4	447	24 AAE33524	Human AQC2 heavy c
25	2191	90.1	449	24 ABP58273	Humanised 3D6 anti
26	2191	90.1	468	24 ABP58275	Humanised 3D6 anti
27	2183.5	89.8	475	13 AAR20057	Heavy chain of 3D6
28	2182	89.7	449	21 AAY68810	A rat heavy chain
29	2178	89.6	474	23 AAO14065	Heavy chain protei
30	2178	89.6	474	24 ABU08017	Human monoclonal r
31	2177.5	89.5	444	24 AAE34876	BIWA4/8 antibody h
32	2177	89.5	451	22 AAE12715	Human recombinant
33	2177	89.5	451	24 ABU58807	Mucin 1 (MUC-1) bi
34	2176.5	89.5	442	24 ABB80109	Heavy chain. Homo
35	2176.5	89.5	442	24 ABR39465	Humanised anti-Abe
36	2176.5	89.5	442	24 ABU08311	Humanised 266 anti
37	2176.5	89.5	461	22 AAU07745	Humanised monoclon
38	2170.5	89.2	449	23 AAO18400	Mature humanised m
39	2169	89.2	582	22 AAB81987	Ganglioside GD3 sp
40	2168.5	89.2	442	24 ABB80113	Deglycosylated hea
41	2168.5	89.2	442	24 ABR39474	Humanised anti-Abe
42	2168.5	89.2	442	24 ABU08320	Humanised antibody
43	2164.5	89.0	459	14 AAR42066	Human anti-HBs hea
44	2161	88.9	464	23 ABG91842	Human antibody fra
45	2161	88.9	464	23 ABG78151	Human Fv molecule

ALIGNMENTS

RESULT 1
AAR33311
ID AAR33311 standard; Protein; 453 AA.
XX
AC AAR33311;
XX
DT 25-MAR-2003 (updated)
DT 05-JUL-1993 (first entry)
XX
DE Humanised MaEl1 Version 1 (intact IgG) heavy chain.
XX
KW Antibody; high affinity; FCEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAEl1; Fab; humael1v1.
XX
OS Synthetic.
XX
PN WO9304173-A1.
XX
PD 04-MAR-1993.
XX
PF 14-AUG-1992; 92WO-US06860.
XX
PR 14-AUG-1991; 91US-0744768.
PR 07-MAY-1992; 92US-0879495.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
DR WPI; 1993-094004/11.
XX

PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
XX
PS Example 4; Fig 3; 113pp; English.
XX
CC Residues were selected from MaE11 and inserted or substituted into
CC a human Fab antibody background (Vh region Kabat subgroup III and VI
CC region kappa subgroup I). A first version, humaellv1 or version 1 is
CC given below. The affinity of version 1 was assayed and found to be
CC ca. 100 times lower than that of the donor antibody MaE11.
CC Therefore, further modifications in the sequence of version 1
CC were made.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 453 AA;

Query Match 100.0%; Score 2432; DB 14; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.5e-144;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db |||||
QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db |||||
QY 61 ADSVKGRFTISRDDSKNTFFYLQMNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLTVTVS 120
Db |||||
QY 61 ADSVKGRFTISRDDSKNTFFYLQMNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLTVTVS 120
Db |||||
QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db |||||
QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db |||||
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db |||||
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db |||||
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db |||||
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db |||||
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db |||||
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db |||||
QY 361 REEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 420
Db |||||
QY 361 REEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 420
Db |||||
QY 421 SRWQOGNVFSCSVMH EALHNHYTQKSLSLSPGK 453
Db |||||
QY 421 SRWQOGNVFSCSVMH EALHNHYTQKSLSLSPGK 453
Db |||||

RESULT 2
AA Y85199
ID AAY85199 standard; protein; 453 AA.
XX
AC AAY85199;
XX
DT 29-JUN-2000 (first entry)
XX
DE Heavy chain amino acid sequence of the humanised MaE11 antibody.
XX
KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FcEL; FCEH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; heavy chain; prevent; chimeric.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN US6037453-A.
XX

PD 14-MAR-2000.
XX
PF 06-JUN-1995; 95US-0466151.
XX
PR 15-MAR-1995; 95US-0405617.
PR 14-AUG-1992; 92WO-US06860.
PR 26-JAN-1994; 94US-0185899.
XX (GETH) GENENTECH INC.
PA Presta LG, Jardieu PM;
XX WPI; 2000-269913/23.
DR
XX
PT New bispecific antibodies, useful for treating immunoglobulin
PT E-mediated disease, binds to IgE, but only when on the low affinity
PT receptor, and to an antigen other than IgE
XX
PS Claim 14; Fig 3; 48pp; English.
XX
CC This sequence represents the heavy chain amino acid sequence of a
CC humanised mouse anti-human immunoglobulin E (IgE) antibody. The invention
CC relates to a bispecific antibody that binds specifically to IgE when IgE
CC is bound to its low affinity receptor (FCEL), but does not bind to IgE,
CC when IgE is bound to its high affinity receptor (FCEH). The bispecific
CC antibody comprises an IgE-binding arm with human framework residues of a
CC recipient human antibody and donor murine CDR (complementarity
CC determining region) residues, but with at least one human CDR residue
CC replacing the analogous murine residue. The antibody also comprises an Fv
CC that is specific for a predetermined antigen other than IgE. The
CC antibodies work by displacing bound IgE from its receptor, or via
CC competitive inhibition of its binding. The bispecific antibodies are used
CC for diagnosis, treatment and prevention of allergy and other IgE-mediated
CC diseases, also, when immobilised, for the isolation of FCEL from cells
CC (for research or therapy). The bispecific antibodies of the invention do
CC not cause granulation or release of histamine from mast cells.
XX
SQ Sequence 453 AA;

Query Match 100.0%; Score 2432; DB 21; Length 453;
Best Local Similarity 100.0%; Pred. No. 3.5e-144;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db |||||
QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db |||||
QY 61 ADSVKGRFTISRDDSKNTFFYLQMNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLTVTVS 120
Db |||||
QY 61 ADSVKGRFTISRDDSKNTFFYLQMNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLTVTVS 120
Db |||||
QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db |||||
QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180
Db |||||
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db |||||
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db |||||
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db |||||
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db |||||
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db |||||
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db |||||
QY 361 REEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 420
Db |||||
QY 361 REEMTKNQVSLTCLVKGFYPSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDK 420
Db |||||
QY 421 SRWQOGNVFSCSVMH EALHNHYTQKSLSLSPGK 453
Db |||||

Db 421 SRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 453

RESULT 3

AAW95659

ID AAW95659 standard; protein; 451 AA.

XX

AC AAW95659;

XX

DT 08-JUN-1999 (first entry)

XX

DE Mus musculus anti-IgE e25 full length variable heavy chain.

XX

KW Heavy chain; IgE; antibody; anti-IgE; reduction; prevention;

KW histamine; production; hypersensitivity; allergen; anaphylaxis;

KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;

KW eczema; anaphylactic shock; urticaria.

XX

OS Mus musculus.

XX

PN WO9901556-A2.

XX

PD 14-JAN-1999.

XX

PF 30-JUN-1998; 98WO-US13410.

XX

PR 02-JUL-1997; 97US-0887352.

XX

PA (GETH) GENENTECH INC.

XX

PI Jardieu PM, Lowe J, Lowman HB, Presta LG;

XX

DR WPI; 1999-106057/09.

XX

PT Improving affinity of polypeptides, particularly anti-IgE antibodies

PT - by identifying aspartyl residues which undergo isomerisation and

PT. substituting alternative residues and screening for affinity against

PT the target

XX

PS Disclosure; Pages 92-94; 129pp; English.

XX

CC The sequence is that of thefull length heavy chain of e25. It

CC was used as part of a method to improve the affinity of anti-IgE

CC antibodies such as e26 and e27. The e26 and e27 antibodies can

CC be used for reducing or preventing IgE mediated production of

CC histamine in a mammal. They can be used for treating a disorder

CC mediated by IgE such as hypersensitivity, atopic allergy, asthma,

CC allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic

CC shock and urticaria. The antibodies can also be used for affinity

CC purification, detection and diagnosis.

XX

SQ Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 20; Length 451;

Best Local Similarity 98.9%; Pred. No. 1.3e-141;

Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYICARGSHYFGHWHFVWGQGLTVTVS 120

Db 61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYICARGSHYFGHWHFVWGQGLTVTVS 120

QY 121 SASTKGKPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180

Db 121 SAST--KGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPEL 240

Db 179 QSSGLYSLSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPEL 238

QY 241 LGGPSVLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300

Db 239 LGGPSVLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360

Db 299 QYNSTYRVVSVLTVHLQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420

Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 453

Db 419 SRWQGNVFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 4

AAW95661

ID AAW95661 standard; protein; 451 AA.

XX

AC AAW95661;

XX

DT 08-JUN-1999 (first entry)

XX

DE Mus musculus anti-IgE e26 full length heavy chain.

XX

KW Heavy chain; IgE; antibody; anti-IgE; reduction; prevention;

KW histamine; production; hypersensitivity; allergen; anaphylaxis;

KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;

KW eczema; anaphylactic shock; urticaria.

XX

OS Mus musculus.

XX

PN WO9901556-A2.

XX

PD 14-JAN-1999.

XX

PF 30-JUN-1998; 98WO-US13410.

XX

PR 02-JUL-1997; 97US-0887352.

XX

PA (GETH) GENENTECH INC.

PI Jardieu PM, Lowe J, Lowman HB, Presta LG;

XX

DR WPI; 1999-106057/09.

XX

PT Improving affinity of polypeptides, particularly anti-IgE antibodies

PT - by identifying aspartyl residues which undergo isomerisation and

PT substituting alternative residues and screening for affinity against

PT the target

XX

PS Disclosure; Pages 95-96; 129pp; English.

XX

CC The sequence is that of the full length heavy chain of e26. It

CC was used as part of a method to improve the affinity of anti-IgE

CC antibodies such as e26 and e27. The e26 and e27 antibodies can

CC be used for reducing or preventing IgE mediated production of

CC histamine in a mammal. They can be used for treating a disorder

CC mediated by IgE such as hypersensitivity, atopic allergy, asthma,

CC allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic

CC shock and urticaria. The antibodies can also be used for affinity

CC purification, detection and diagnosis.

XX

SQ Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 20; Length 451;

Best Local Similarity 98.9%; Pred. No. 1.3e-141;

Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

|||||

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNWIRQAPGKGLEWVASITYDGSSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

Db 61 NPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180

Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 240

Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300

Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360

Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420

Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 453

Db 419 SRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 5

AAY85201

ID AAY85201 standard; protein; 451 AA.

XX

AC AAY85201;

XX

DT 29-JUN-2000 (first entry)

XX

DE Light chain amino acid sequence of anti-human IgE antibody.

XX

KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH; low affinity binding receptor; high affinity binding receptor; allergy; diagnosis; treatment; histamine release; heavy chain; prevent.

KW

XX

OS Mus sp.

XX

PN US6037453-A.

XX

PD 14-MAR-2000.

XX

PF 06-JUN-1995; 95US-0466151.

XX

PR 15-MAR-1995; 95US-0405617.

PR 14-AUG-1992; 92WO-US06860.

PR 26-JAN-1994; 94US-0185899.

XX

PA (GETH) GENENTECH INC.

XX

PI Presta LG, Jardieu PM;

XX

DR WPI; 2000-269913/23.

XX

PT New bispecific antibodies, useful for treating immunoglobulin

PT E-mediated disease, binds to IgE, but only when on the low affinity

PT receptor, and to an antigen other than IgE

XX

PS Claim 15; Column 73-76; 48pp; English.

XX

CC This sequence represents the light chain amino acid sequence of a mouse

CC anti-human immunoglobulin E (IgE) antibody. The invention relates to a

CC bispecific antibody that binds specifically to IgE when IgE is bound to

CC its low affinity receptor (FCEL), but does not bind to IgE, when IgE is

CC bound to its high affinity receptor (FCEH). The bispecific antibody

CC comprises an IgE-binding arm with human framework residues of a recipient

CC human antibody and donor murine CDR (complementarity determining region)

CC residues, but with at least one human CDR residue replacing the analogous

CC murine residue. The antibody also comprises an Fv that is specific for a

CC predetermined antigen other than IgE. The antibodies work by displacing

CC bound IgE from its receptor, or via competitive inhibition of its

CC binding. The bispecific antibodies are used for diagnosis, treatment and

CC prevention of allergy and other IgE-mediated diseases, also, when

CC immobilised, for the isolation of FCEL from cells (for research or

CC therapy). The bispecific antibodies of the invention do not cause

CC granulation or release of histamine from mast cells.

XX SQ Sequence 451 AA;

Query Match 98.3%; Score 2391; DB 21; Length 451;

Best Local Similarity 98.9%; Pred. No. 1.3e-141;

Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNWIRQAPGKGLEWVASITYDGSSTNY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNWIRQAPGKGLEWVASITYDGSSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

Db 61 NPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180

Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 240

Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300

Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360

Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420

Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 453

Db 419 SRWQQGNVFSCSVMHAEALHNHYTQKSLSLSPGK 451

RESULT 6

AAB47088

ID AAB47088 standard; protein; 451 AA.

XX

AC AAB47088;

XX

DT 08-MAY-2001 (first entry)

XX

DE Anti-IgE antibody, E26, heavy chain.

XX

KW Light chain; heavy chain; anti-IgE antibody; E26; transfection;

KW green fluorescent protein; GFP; promoter; expression.

XX

OS Chimeric - Homo sapiens.

OS Chimeric - Mus musculus.

XX

PN WO200104306-A1..

XX

PD 18-JAN-2001.

XX

PF 11-JUL-2000; 2000WO-US18841.

Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFSCSVMHREALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSCSVMHREALHNHYTQKSLSLSPGK 451

RESULT 8
AAB76950
ID AAB76950 standard; Protein; 451 AA.
XX
AC AAB76950;
XX
DT 17-APR-2001 (first entry)
XX
DE Full length heavy chain sequence of e26 SEQ ID 16.
DE

KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.

OS Synthetic.
XX
XX US6172213-B1.
XX
PD 09-JAN-2001.
XX
PF 30-JUN-1998; 98US-0109207.
XX
PR 02-JUL-1997; 97US-0051554.
XX

PA (GETH) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
DR WPI; 2001-122353/13.

XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display
XX
PS Claim 2; Fig 12; 87pp; English.

XX This invention relates to a nucleotide sequence encoding an antibody
CC with improved anti-IgE antibody activity. The antibody has improved
CC action due to a process comprising, a) identifying aspartyl residues
CC prone to isomerisation in unimproved anti-IgE (immunoglobulin E)
CC antibody; b) substituting alternative residues to create candidate
CC molecules, and c) selecting those candidate molecules which display
CC affinity against the target molecule. Use of the antibody results in
CC antiasthmatic; antiallergic; ophthalmological; dermatological and
CC antiinflammatory activity. The antibodies are useful for treating
CC IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis,
CC eczema, urticaria and food allergies. The mutant antibodies produced by
CC the above mentioned nucleic acids may also be used as affinity
CC purification agents and in diagnostic assays for detecting the expression
CC of an antigen of interest in specific cell, tissues or serum. Amino acid
CC sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of
CC the invention. Polynucleotide sequence AAF69253 represents an expression

CC plasmid used in the course of the invention, and oligonucleotides
CC AAF69254 - AAF69271 are used in the generation of affinity improved
CC anti-IgE antibodies.
XX
SQ Sequence 451 AA;
Query Match 98.3%; Score 2391; DB 22; Length 451;
Best Local Similarity 98.9%; Pred. No. 1.3e-141;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHEFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHEFAVWGQGLTVTVS 120
QY 121 SASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQGNVFSCSVMHREALHNHYTQKSLSLSPGK 453
Db 419 SRWQGNVFSCSVMHREALHNHYTQKSLSLSPGK 451

RESULT 9
AAY50031
ID AAY50031 standard; protein; 451 AA.
XX
AC AAY50031;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human E27 anti-IgE antibody heavy chain.
XX
KW Immunoglobulin E; IgE; antibody; vascular endothelial growth factor;
KW VEGF; chimeric; IgG; assay; Fc gamma receptor; low affinity; hexamer;
KW complex; cross-linked; enzyme-linked immunosorbent assay; ELISA;
KW heavy chain.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9951642-A1.
XX
PD 14-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US06858.
PR 02-APR-1998; 98US-0054255.
PR 15-JAN-1999; 99US-0116100.
XX
PA (GETH) GENENTECH INC.
XX
PI Idusogie EE, Mulkerrin MG, Presta LG, Shields RL;

Db 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 453

Db 419 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 451

RESULT 11

AAB07473

ID AAB07473 standard; protein; 451 AA.

XX AC AAB07473;

XX 20-OCT-2000 (first entry)

DE Amino acid sequence of E27 and anti-IgE antibody heavy chain.

XX anti-IgE antibody; heavy chain; Fc region; effector function; cancer;

KW allergy; asthma; LFA-1-mediated disorder; tumour; cancer.

XX OS Synthetic.

XX WO200042072-A2.

PN 20-JUL-2000.

XX 14-JAN-2000; 2000WO-US00973.

XX 15-JAN-1999; 99US-0116023.

XX (GETH) GENENTECH INC.

XX Presta LG;

PI WPI; 2000-476035/41.

DR New Fc region-containing polypeptides that have altered effector

XX function due to one or more amino acid modifications in the Fc region,

PT useful in the treatment of cancer and allergic conditions such as

PT asthma

XX Disclosure; Fig 4B; 132pp; English.

PS The present sequence represents the E27 and anti-IgE antibody heavy

XX chain. The protein is used to produce Fc region-containing polypeptides

CC that have altered effector function as a consequence of one or more

CC amino acid modifications in the Fc region. The variant polypeptides are

CC useful for treating cancer, allergic conditions such as asthma (with an

CC anti-IgE antibody), and LFA-1-mediated disorders. Where the polypeptide

CC binds the HER2 receptor, the disorder preferably is HER2-expressing

CC cancer, e.g. a benign or malignant tumour characterized by overexpression

CC of the HER2 receptor. Such cancers include breast cancer, squamous cell

CC cancer, small-cell lung cancer, non-small cell lung cancer,

CC gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical

CC cancer, ovarian cancer, bladder cancer, hepatoma, colon cancer,

CC colorectal cancer, endometrial carcinoma, salivary gland carcinoma,

CC kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid

CC cancer, hepatic carcinoma and various types of head and neck cancer.

XX SQ Sequence 451 AA;

Query Match 97.4%; Score 2369; DB 21; Length 451;

Best Local Similarity 98.0%; Pred. No. 3e-140;

Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps. 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYGETKY 60

QY 61 ADSVKGRFTISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

Db 61 NPSVKGRITISRDDSKNTFYQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 180

Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 240

Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300

Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360

Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 420.

Db 359 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 453

Db 419 SRWQGNVFCSCVMHEALHNHYTKLSLSPGK 451

RESULT 12

AAB74212

ID AAB74212 standard; protein; 451 AA.

XX AC AAB74212;

XX 17-MAY-2001 (first entry)

DE E27 anti-IgE antibody heavy chain.

XX Antibody; antigen; cancer; allergy; asthma; LFA-mediated;

KW autoimmune; vasculitis.

XX Unidentified.

XX US6194551-B1.

XX 27-FEB-2001.

XX 31-MAR-1999; 99US-0282505.

XX 02-APR-1998; 98US-0080447.

XX (GETH) GENENTECH INC.

PI Idusogie EE, Presta LG, Mulkerrin MG;

XX WPI; 2001-217935/22.

XX Novel polypeptide variant useful for treating cancers, allergic

PT diseases such as asthma and autoimmune diseases, comprises human

PT immunoglobulin-G Fc region, retains the ability to bind antigen and

PT does not activate complement

XX Disclosure; Fig 4; 30pp; English.

XX The present invention relates to a variant of an antibody

CC having a human immunoglobulin (Ig)G Fc region, with an

CC amino acid substitution. The mutant retains the ability to

CC bind antigen. The invention is useful for determining the

CC presence of a protein of interest, by exposing the sample

CC suspected of containing the protein to the antibody and

CC determining the binding of it to the sample. The antibody

CC is also useful for treating cancer, allergic conditions

CC including asthma, LFA-mediated disorders, autoimmune

XX disorders and vasculitis.

XX Sequence 451 AA;

QY	239	ELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR	298
Db			
Db	238	ELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR	297
QY	299	EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP	358
Db			
Db	298	EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP	357
QY	359	PSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV	418
Db			
Db	358	PSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV	417
QY	419	DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	453
Db			
Db	418	DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	452

Search completed: August 12, 2003, 16:30:04
Job time : 56.3338 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:28:52 ; Search time 19.5782 Seconds
(without alignments)
978.986 Million cell updates/sec

Title: US-09-802-077-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2432	100.0	453	3	US-08-466-151-8
2	2432	100.0	453	4	US-08-466-163B-8
3	2391	98.3	451	2	US-08-887-352B-14
4	2391	98.3	451	2	US-08-887-352B-16
5	2391	98.3	451	3	US-08-466-151-65
6	2391	98.3	451	3	US-09-109-207C-14
7	2391	98.3	451	3	US-09-109-207C-16
8	2391	98.3	451	3	US-09-296-005-14
9	2391	98.3	451	3	US-09-296-005-16
10	2369	97.4	451	2	US-08-887-352B-18
11	2369	97.4	451	3	US-09-109-207C-18
12	2369	97.4	451	3	US-09-282-505-2
13	2369	97.4	451	3	US-09-054-255-2
14	2369	97.4	451	3	US-09-296-005-18
15	2369	97.4	451	4	US-09-282-846-2
16	2369	97.4	451	4	US-09-680-145-2
17	2214.5	91.1	452	3	US-09-027-449-71
18	2214.5	91.1	452	3	US-09-026-985-71
19	2214.5	91.1	452	4	US-09-121-952A-71
20	2214.5	91.1	452	4	US-09-234-340A-71
21	2179.5	89.6	449	4	US-09-679-397-2
22	2179.5	89.6	449	4	US-09-680-148-2
23	2179.5	89.6	449	4	US-09-304-465A-2
24	2164.5	89.0	459	1	US-08-157-101A-7
25	2132	87.7	478	3	US-08-487-550-8
26	2132	87.7	478	4	US-09-526-098-8
27	2117.5	87.1	473	3	US-09-049-672A-4

28	2093	86.1	476	3	US-08-487-550-12	Sequence 12, Appl
29	2093	86.1	476	4	US-09-526-098-12	Sequence 12, Appl
30	2092	86.0	449	1	US-08-458-516-13	Sequence 13, Appl
31	2078	85.4	472	4	US-08-793-450-8	Sequence 8, Appli
32	2073.5	85.3	446	3	US-08-397-411-7	Sequence 7, Appli
33	2069	85.1	468	4	US-09-485-737B-67	Sequence 67, Appl
34	2069	85.1	476	3	US-08-487-550-4	Sequence 4, Appli
35	2069	85.1	476	4	US-09-526-098-4	Sequence 4, Appli
36	2069	85.1	711	4	US-09-485-737B-90	Sequence 90, Appl
37	2056.5	84.6	467	3	US-09-049-672A-8	Sequence 8, Appli
38	2056.5	84.6	475	4	US-09-740-002-27	Sequence 27, Appl
39	2052.5	84.4	467	1	US-08-704-744-81	Sequence 81, Appl
40	2047	84.2	443	5	PCT-US96-13152-4	Sequence 4, Appli
41	2036	83.7	472	4	US-09-301-593-43	Sequence 43, Appl
42	2032	83.6	451	4	US-09-247-352-3	Sequence 3, Appli
43	2032	83.6	451	4	US-09-466-635-3	Sequence 3, Appli
44	2029	83.4	476	2	US-08-378-939-10	Sequence 10, Appl
45	2021.5	83.1	453	4	US-09-301-593-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid

Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSWNIQAPGKLEWVASITYDGSTNY 60
|||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSWNIQAPGKLEWVASITYDGSTNY 60
|||||

QY 61 ADSVKGRFTISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVTS 120
|||||
Db 61 NPSVKGRITISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVTS 120
|||||

QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
|||||
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
|||||

QY 181 QSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
|||||
Db 179 QSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
|||||

QY 241 LGGPSVFELPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
|||||
Db 239 LGGPSVFELPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
|||||

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
|||||
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
|||||

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
|||||
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
|||||

QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
|||||
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
|||||

RESULT 4
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-16

Query Match 98.3%; Score 2391; DB 2; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSWNIQAPGKLEWVASITYDGSTNY 60
|||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSWNIQAPGKLEWVASITYDGSTNY 60
|||||

QY 61 ADSVKGRFTISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVTS 120
|||||
Db 61 NPSVKGRITISRDDSKNTFY LQMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVTS 120
|||||

QY 121 SASTKGKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
|||||
Db 121 SAST--KGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
|||||

QY 181 QSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
|||||
Db 179 QSSGLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
|||||

QY 241 LGGPSVFELPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
|||||
Db 239 LGGPSVFELPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
|||||

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
|||||
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
|||||

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
|||||
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
|||||

QY 421 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
|||||
Db 419 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
|||||

RESULT 5
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495

```
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-65

Query Match          98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVMHREALNHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHREALNHNHYTQKSLSLSPGK 451

RESULT 6
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match          98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
```

```
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match          98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVMHREALNHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHREALNHNHYTQKSLSLSPGK 451

RESULT 7
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16

Query Match          98.3%; Score 2391; DB 3; Length 451;
Best Local Similarity 98.9%; Pred. No. 3.9e-181;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
```


Db 419 SRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 451

RESULT 10

US-08-887-352B-18
; Sequence 18, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-18.

Query Match 97.4%; Score 2369; DB 2; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.le-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY	1	EVQLVESGGGLVQPGGSLRLSCA	VSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCA	VSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY	60
QY	61	ADSVKGRFTISRDDSKNTFY	LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS	120
Db	61	NPSVKGRITISRDDSKNTFY	LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS	120
QY	121	SASTKGKPSVFPLAPSSKST	SGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	180
Db	121	SAST--KGPSVFPLAPSSKST	SGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	178
QY	181	QSSGLYSLSVTVTPSSSLGT	QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL	240
Db	179	QSSGLYSLSVTVTPSSSLGT	QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL	238
QY	241	LGGPSVFLFPPKPKDTLMIS	RTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	300
Db	239	LGGPSVFLFPPKPKDTLMIS	RTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	298
QY	301	QYNSTYRVVSVLTVLHQD	WLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	360
Db	299	QYNSTYRVVSVLTVLHQD	WLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	358
QY	361	REEMTKNQVSLTCLVKGF	YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK	420
Db	359	REEMTKNQVSLTCLVKGF	YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK	418

QY	421	SRWQGNVFCSCVMHEALHNHY	TQKSLSLSPGK	453
Db	419	SRWQGNVFCSCVMHEALHNHY	TQKSLSLSPGK	451

RESULT 11

US-09-109-207C-18
; Sequence 18, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:

; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11

US-09-109-207C-18

Query Match 97.4%; Score 2369; DB 3; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.le-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY	1	EVQLVESGGGLVQPGGSLRLSCA	VSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY	60
Db	1	EVQLVESGGGLVQPGGSLRLSCA	VSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY	60
QY	61	ADSVKGRFTISRDDSKNTFY	LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS	120
Db	61	NPSVKGRITISRDDSKNTFY	LQMNLSRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTS	120
QY	121	SASTKGKPSVFPLAPSSKST	SGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	180
Db	121	SAST--KGPSVFPLAPSSKST	SGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL	178
QY	181	QSSGLYSLSVTVTPSSSLGT	QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL	240
Db	179	QSSGLYSLSVTVTPSSSLGT	QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL	238
QY	241	LGGPSVFLFPPKPKDTLMIS	RTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	300
Db	239	LGGPSVFLFPPKPKDTLMIS	RTPETVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	298
QY	301	QYNSTYRVVSVLTVLHQD	WLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	360
Db	299	QYNSTYRVVSVLTVLHQD	WLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS	358
QY	361	REEMTKNQVSLTCLVKGF	YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK	420
Db	359	REEMTKNQVSLTCLVKGF	YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK	418
QY	421	SRWQGNVFCSCVMHEALHNHY	TQKSLSLSPGK	453
Db	419	SRWQGNVFCSCVMHEALHNHY	TQKSLSLSPGK	451

RESULT 12

US-09-282-505-2
; Sequence 2, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:

; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants

QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHREALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHREALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-282-846-2
; Sequence 2, Application: US/09282846
; Patent No. 6528624
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R2
; CURRENT APPLICATION NUMBER: US/09/282,846
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6528624
US-09-282-846-2

Query Match 97.4%; Score 2369; DB 4; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.1e-179;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS TNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY 60
QY 61 ADSVKGRFTISRDDSKNTFY LQMNSLR AEDTAVYYCARGSHYFGHW HFAVWGQGLTVTS 120
Db 61 NPSVKGRITISRDDSKNTFY LQMNSLR AEDTAVYYCARGSHYFGHW HFAVWGQGLTVTS 120
QY 121 SASTKGKPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAA LGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420

Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHREALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHREALHNHYTQKSLSLSPGK 451
Search completed: August 12, 2003, 16:32:54
Job time : 21.5782 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

```
Run on:      August 12, 2003, 16:31:48 ; Search time 48.608 Seconds
              (without alignments)
              1186.320 Million cell updates/sec
```

Title: US-09-802-077-8
 Perfect score: 2432
 Sequence: 1 EVQLVESGGGLVQGGSLRL.....MHEALHNHYTOKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 479057 seqs, 127295195 residues

Total number of hits satisfying chosen parameters: 479057

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	2432	100.0	453	9	US-09-802-077-8		Sequence 8, Appli
2	2432	100.0	453	9	US-09-802-096-8		Sequence 8, Appli
3	2432	100.0	453	11	US-09-925-179-8		Sequence 8, Appli
4	2391	98.3	451	9	US-09-920-171-14		Sequence 14, Appl
5	2391	98.3	451	9	US-09-920-171-16		Sequence 16, Appl
6	2391	98.3	451	11	US-09-925-179-65		Sequence 65, Appl
7	2388	98.2	451	11	US-09-925-179-66		Sequence 66, Appl
8	2379	97.8	451	11	US-09-925-179-68		Sequence 68, Appl
9	2369	97.4	451	9	US-09-920-171-18		Sequence 18, Appl
10	2214.5	91.1	452	11	US-09-726-258-71		Sequence 71, Appl
11	2210	90.9	476	15	US-10-020-786-11		Sequence 11, Appl
12	2182	89.7	449	10	US-09-736-371B-21		Sequence 21, Appl
13	2179.5	89.6	449	15	US-10-253-366-2		Sequence 2, Appli
14	2179.5	89.6	449	15	US-10-316-694-2		Sequence 2, Appli
15	2177.5	89.5	444	15	US-10-150-475A-6		Sequence 6, Appli

16	2177	89.5	451	10	US-09-822-698A-26	Sequence 26, Appl
17	2148	88.3	470	15	US-10-020-786-9	Sequence 9, Appli
18	2148	88.3	470	15	US-10-227-694-5	Sequence 5, Appli
19	2132	87.7	478	10	US-09-948-429B-8	Sequence 8, Appli
20	2132	87.7	478	14	US-10-124-905-8	Sequence 8, Appli
21	2119	87.1	470	15	US-10-216-484-157	Sequence 157, App
22	2108	86.7	470	15	US-10-216-484-147	Sequence 147, App
23	2107	86.6	470	15	US-10-216-484-145	Sequence 145, App
24	2105	86.6	470	15	US-10-216-484-143	Sequence 143, App
25	2102	86.4	470	15	US-10-216-484-117	Sequence 117, App
26	2094	86.1	470	15	US-10-216-484-89	Sequence 89, Appl
27	2093	86.1	476	10	US-09-948-429B-12	Sequence 12, Appl
28	2093	86.1	476	14	US-10-124-905-12	Sequence 12, Appl
29	2088.5	85.9	731	10	US-09-825-012-46	Sequence 46, Appl
30	2088.5	85.9	741	10	US-09-825-012-55	Sequence 55, Appl
31	2083.5	85.7	729	10	US-09-825-012-52	Sequence 52, Appl
32	2083.5	85.7	739	10	US-09-825-012-61	Sequence 61, Appl
33	2077.5	85.4	730	10	US-09-825-012-49	Sequence 49, Appl
34	2077.5	85.4	740	10	US-09-825-012-58	Sequence 58, Appl
35	2069	85.1	468	15	US-10-071-485-67	Sequence 67, Appl
36	2069	85.1	476	10	US-09-948-429B-4	Sequence 4, Appli
37	2069	85.1	476	14	US-10-124-905-4	Sequence 4, Appli
38	2069	85.1	711	15	US-10-071-485-90	Sequence 90, Appl
39	2068.5	85.1	450	9	US-09-796-848A-43	Sequence 43, Appl
40	2068.5	85.1	450	10	US-09-996-288-218	Sequence 218, App
41	2068.5	85.1	450	10	US-09-996-288-250	Sequence 250, App
42	2068.5	85.1	450	11	US-09-996-265-218	Sequence 218, App
43	2068.5	85.1	450	11	US-09-996-265-250	Sequence 250, App
44	2068	85.0	476	10	US-09-747-669-3	Sequence 3, Appli
45	2068	85.0	476	15	US-10-290-703-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1

```

US-09-802-077-8
; Sequence 8, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Al
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, vers
US-09-802-077-8

```

	Query Match	100.0%;	Score 2432;	DB 9;	Length 453;
	Best Local Similarity	100.0%;	Pred. No. 1e-162;		
	Matches 453; Conservative	0;	Mismatches	0;	Gaps 0
QY	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIROAPGKGLEWVASITYDGS	TNY	60	
Dd	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIROAPGKGLEWVASITYDGS	TNY	60	

Db 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
QY 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
Db 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
QY 421 SRWQQGNVFSCSVMHREALHNYHTQKSLSLSPGK 453
Db 421 SRWQQGNVFSCSVMHREALHNYHTQKSLSLSPGK 453

RESULT 4

US-09-920-171-14
; Sequence 14, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-14

Query Match 98.3%; Score 2391; DB 9; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.5e-160;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFVWGQGTLLTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFVWGQGTLLTVS 120
QY 121 SASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
Db 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHREALHNYHTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHREALHNYHTQKSLSLSPGK 451

RESULT 5

US-09-920-171-16
; Sequence 16, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-16

Query Match 98.3%; Score 2391; DB 9; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.5e-160;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
QY 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFVWGQGTLLTVS 120
Db 61 NPSVKGRITISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFVWGQGTLLTVS 120
QY 121 SASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178
QY 181 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238
QY 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS 358
QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418
QY 421 SRWQQGNVFSCSVMHREALHNYHTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHREALHNYHTQKSLSLSPGK 451

RESULT 6

US-09-925-179-65
; Sequence 65, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 65
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8b of Tabl
US-09-925-179-65

Query Match 98.3%; Score 2391; DB 11; Length 451;
Best Local Similarity 98.9%; Pred. No. 7.5e-160;
Matches 448; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFY LQMNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSVKGRITISRDDSKNTFY LQMNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVMHREALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHREALHNHYTQKSLSLSPGK 451

RESULT 7
US-09-925-179-66
; Sequence 66, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:

; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 66
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)8a of T
US-09-925-179-66

Query Match 98.2%; Score 2388; DB 11; Length 451;
Best Local Similarity 98.7%; Pred. No. 1.2e-159;
Matches 447; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNY 60

QY 61 ADSVKGRFTISRDDSKNTFY LQMNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLTVTVS 120
Db 61 NPSLKGRTISRDDSKNTFY LQMNSLRAEDTAVYVCARGSHYFGHWHFAVWGQGLTVTVS 120

QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
Db 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 360
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 420
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQQGNVFSCSVMHREALHNHYTQKSLSLSPGK 453
Db 419 SRWQQGNVFSCSVMHREALHNHYTQKSLSLSPGK 451

RESULT 8
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US


```
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 68
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Table
US-09-925-179-68

Query Match          97.8%; Score 2379; DB 11; Length 451;
Best Local Similarity 97.8%; Pred. No. 5.2e-159;
Matches 443; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSINY 60
   |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSINY 60
   |||||

QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVTS 120
   |||||
Db 61 NDSLKGRITVSRDDSKNTFYIQMNSARAEDTAVYYCARGSHYFGHWFAVWGQGLTVTS 120
   |||||

QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
   |||||
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
   |||||
Db 179 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
   |||||
Db 239 LGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 360
   |||||
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
   |||||
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQOGNVFSCSVMHREALHNYTQKSLSLSPGK 453
   |||||
Db 419 SRWQOGNVFSCSVMHREALHNYTQKSLSLSPGK 451

RESULT 9
US-09-920-171-18
; Sequence 18, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
```

```
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 18
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-920-171-18

Query Match          97.4%; Score 2369; DB 9; Length 451;
Best Local Similarity 98.0%; Pred. No. 2.6e-158;
Matches 444; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSINY 60
   |||||
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASIKYSGETKY 60
   |||||

QY 61 ADSVKGRFTISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVTS 120
   |||||
Db 61 NPSVKGRITISRDDSKNTFYIQMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVTS 120
   |||||

QY 121 SASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
   |||||
Db 121 SAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

QY 181 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
   |||||
Db 179 QSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 238

QY 241 LGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300
   |||||
Db 239 LGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298

QY 301 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 360
   |||||
Db 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 358

QY 361 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 420
   |||||
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418

QY 421 SRWQOGNVFSCSVMHREALHNYTQKSLSLSPGK 453
   |||||
Db 419 SRWQOGNVFSCSVMHREALHNYTQKSLSLSPGK 451

RESULT 10
US-09-726-258-71
; Sequence 71, Application US/09726258
; Publication No. US20030021790A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
; TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
```


Job time : 50.608 secs

Db 295 REEQNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 354
QY 358 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT 417
Db 355 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLT 414
QY 418 VDKSRWQQGNVFSCSVMHREALHNNHYTQKSLSPG 452
Db 415 VDKSRWQQGNVFSCSVMHREALHNNHYTQKSLSPG 449

RESULT 15
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

Query Match 89.5%; Score 2177.5; DB 15; Length 444;
Best Local Similarity 91.2%; Pred. No. 6.8e-145;
Matches 415; Conservative 16; Mismatches 11; Indels 13; Gaps 5;
QY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59
Db 1 EVQLVESGGGLVQPGGSLRLSCA AAGTFSS-YDMSWVRQAPGKGLEWVSTISSGGSYTY 59
QY 60 YADSVKGRFTISRDDSKNFTY LQMNSLRAEDTAVYYCAR-GSHYFGHWHFVWVGQGT LVT 118
Db 60 YLDSIKGRFTISRDNAKNSLY LQMNSLRAEDTAVYYCARQGLDY-----WGRGTLVT 111
QY 119 VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
Db 112 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 169
QY 179 VLQSSGLYSLSSVTVPSSSLGTQTY ICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAP 238
Db 170 VLQSSGLYSLSSVTVPSSSLGTQTY ICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAP 229
QY 239 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
Db 230 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 289
QY 299 EEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 358
Db 290 EEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 349
QY 359 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV 418
Db 350 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTV 409
QY 419 DKSRWQQGNVFSCSVMHREALHNNHYTQKSLSPGK 453
Db 410 DKSRWQQGNVFSCSVMHREALHNNHYTQKSLSPGK 444

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:26:07 ; Search time 20.2534 Seconds
(without alignments)
2150.973 Million cell updates/sec

Title: US-09-802-077-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query		Description	
No.	Score	Match	Length	ID	
1	1750	72.0	330	1 GHHU	Ig gamma-1 chain C
2	1625.5	66.8	377	2 A23511	Ig gamma-3 chain C
3	1623.5	66.8	377	2 A60764	Ig gamma-3 chain C
4	1599	65.7	326	1 G2HU	Ig gamma-2 chain C
5	1585.5	65.2	327	1 G4HU	Ig gamma-4 chain C
6	1507.5	62.0	444	2 PC4436	monoclonal antibod
7	1477	60.7	374	2 S69339	Ig heavy chain V r
8	1467	60.3	470	2 S22080	Ig heavy chain pre
9	1444	59.4	472	2 S31459	Ig gamma-1 chain -
10	1403.5	57.7	469	2 S37483	Ig gamma-2a chain
11	1403	57.7	446	2 S40295	Ig gamma-2a chain
12	1359	55.9	474	1 G2MS11	Ig gamma-2b chain
13	1345.5	55.3	475	2 S01321	Ig gamma-2a chain
14	1263	51.9	328	2 I47159	Ig gamma 2a chain
15	1257	51.7	328	2 I47160	Ig gamma 2b chain
16	1254	51.6	255	4 S31866	Ig gamma-1 chain C
17	1248.	51.3	234	2 PT0207	Ig gamma chain C r
18	1231.5	50.6	323	1 GHRB	Ig gamma chain C r
19	1231	50.6	328	2 I47158	Ig gamma 1 chain c
20	1227	50.5	328	2 I47161	Ig gamma 3 chain c
21	1202.5	49.4	329	1 G2GP	Ig gamma-2 chain C
22	1162.5	47.8	308	2 C30554	Ig heavy chain C r
23	1157	47.6	289	1 G3HUWI	Ig gamma-3 heavy c
24	1150	47.3	326	2 PS0017	Ig gamma-1 chain C
25	1142	47.0	324	1 G1MS	Ig gamma-1 chain C
26	1142	47.0	329	1 G3MSC	Ig gamma-3 chain C
27	1139.5	46.9	333	2 PS0018	Ig gamma-2b chain
28	1137	46.8	393	1 G1MSM	Ig gamma-1 chain C
29	1131	46.5	398	1 G3MSM	Ig gamma-3 chain C

SUMMARIES

ALIGNMENTS

RESULT 1

GHHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238; PMID:6287432

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Gim(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943; PMID:6811139

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024; PMID:5489771

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: this sequence has the Glm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025; PMID:5530842

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A:Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',27
A;Note: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96,'R',98-197,'D',199-238,'E',240,'M',242-266,'D',268-271,'D',273-330 <SCH
A;Note: this sequence has the Glm(3) and Glm(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 72.0%; Score 1750; DB 1; Length 330;
Best Local Similarity 98.8%; Pred. No. 8.4e-95;
Matches 328; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPEL 241
Db 59 SSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPPEL 118

QY 242 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
Db 119 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 178

QY 302 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
Db 179 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 238

QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS 421
Db 239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS 298

QY 422 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 299 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 1625.5; DB 2; Length 377;
Best Local Similarity 82.1%; Pred. No. 1.7e-87;
Matches 311; Conservative 8; Mismatches 11; Indels 49; Gaps 2;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKV----- 221
Db 59 SSGLYSLSSVTVPPSSSLGTQTYTCNVNHKPSNTKVDKRVELKTPGLDTHTCPRCPEPK 118

QY 222 -----EPKSCDKTHCTCPPELGGPSVFLFPPKPK 254
Db 119 SCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPELGGPSVFLFPPKPK 178

QY 255 DTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 314
Db 179 DTLMSRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 238

QY 315 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCL 374
Db 239 LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCL 298

QY 375 VKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 434
Db 299 VKGFYPSDIAVEWESNGQPENNYTTTPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVM 358

QY 435 HEALHNHYTQKSLSLSPGK 453
Db 359 HEALHNRTQKSLSLSPGK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C;Accession: A60764
R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 1623.5; DB 2; Length 377;
Best Local Similarity 82.1%; Pred. No. 2.2e-87;
Matches 311; Conservative 8; Mismatches 11; Indels 49; Gaps 2;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSGGTAALGLCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNPKSNTKVDKKV----- 221
Db 59 SSGLYSLSSVVTVPSSSLGTQTYTCNVNPKSNTKVDKRVELKTLPLGDTHTCPRCPEPK 118

QY 222 -----EPKSCDKTHTCPPCPAPELGGPSVFLFPPKPK 254
Db 119 SCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPELGGPSVFLFPPKPK 178

QY 255 DTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 314
Db 179 DTLMISRTPEVTCVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 238

QY 315 LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTTLPSSREEMTKNQVSLTCL 374
Db 239 LHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTTLPSSREEMTKNQVSLTCL 298

QY 375 VKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQOGNVFSCSVM 434
Db 299 VKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQOGNVFSCSVM 358

QY 435 HEALHNHYTQKSLSLSPGK 453
Db 359 HEALHNRTQKSLSLSPGK 377

RESULT 4
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A;Reference number: A93906; MUID:82197621; PMID:6804948
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A;Reference number: A93132; MUID:80114419; PMID:118920
A;Contents: Zie
A;Accession: A93132

A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
Submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A;Title: Structural studies of immunoglobulin G.
A;Reference number: A93157; MUID:69064124; PMID:5782707
A;Contents: annotation; Sa, disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG2
A;Cross-references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; heterotetramer; immunoglobulin
C;Keywords: duplication; glycoprotein; immunoglobulin homology
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.7%; Score 1599; DB 1; Length 326;
Best Local Similarity 91.3%; Pred. No. 4.9e-86;
Matches 303; Conservative 10; Mismatches 13; Indels 6; Gaps 3;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSESTAALGLCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNPKSNTKVDKKVEPKSCDKTHTCPCPAPELL 241
Db 59 SSGLYSLSSVVTVPSSNFGTQTYTCNVDPKPSNTKVDKTVERKCCVE---CPPCPAPP-V 114

QY 242 GGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
Db 115 AGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQ 174

QY 302 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 361
Db 175 FNSTFRVVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSR 234

QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKS 421
Db 235 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKS 294

QY 422 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 295 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299662

Db 374 LAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTSQLDADGSYFLYS 433
QY 415 KLTVDKSRWQOQGNVFCSCVMHEALHNHYTKSLSPGK 453
Db 434 RLRVDKNSWQEGDTYACVVMHEALHNHYTKSISKPPGK 472

RESULT 10
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 57.7%; Score 1403.5; DB 2; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.7e-74;
Matches 270; Conservative 68; Mismatches 102; Indels 23; Gaps 8;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASI-TYDGSIN 59
Db 20 QIQLQSGPELVKPGASVKISCKASGYTFTD-YINWVKQKPGQGLKWIYPASGNTK 78
QY 60 YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGS-----HYFGHWHFAVWG 112
Db 79 YNEFKGKATLTVDTSSTAYMQLSSLTSEDNAVYFCARAMGATATLLDY-----WG 130
QY 113 QGTLVTSSASPKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALTSG 172
Db 131 QGTTLTVSSAKT--TAPSVYPLAPVCGDGTGSSVTGLCLVKGYFPEPPTLTWNSGSLSSG 188
QY 173 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTC 232
Db 189 VHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPC 246
QY 233 PP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 290
Db 247 PPKCKAPNLLGGPSVFIFFPKIKDVLMLISLSPVITCVVVDVSEDDPDVQISWFWNVEV 306
QY 291 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTISKAKGQPR 350
Db 307 HTAQTQTHREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIERTISKPKGSVR 366
QY 351 EPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF 410
Db 367 APQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGYS 426
QY 411 FLYSKLTVDKSRWQOQGNVFCSCVMHEALHNHYTKSLSPGK 453
Db 427 FMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTKSFSTRTPGK 469

RESULT 11
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bl
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295

A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CH1>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 57.7%; Score 1403; DB 2; Length 446;
Best Local Similarity 59.4%; Pred. No. 1.7e-74;
Matches 271; Conservative 67; Mismatches 104; Indels 14; Gaps 8;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS--T 58
Db 1 QIQLQSGPELVKPGASVKISCKASGYTFTD-YIHWVKQRPGGLEWIGWI-YPGSGNT 58
QY 59 NYADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLVT 118
Db 59 KYNEFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARG---GKFAMDYWGQGTSVT 114
QY 119 VSSASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALTSGVHTFPA 178
Db 115 VSSAKT--TAPSVYPLAPVCGDGTGSSVTGLCLVKGYFPEPPTLTWNSGSLSSGVHTFPA 172
QY 179 VLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCPP--CP 236
Db 173 VLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCP 230
QY 237 APPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 296
Db 231 APNLLGGPSVFIFFPKIKDVLMLISLSPMVTCTVVVDVSEDDPDVQISWFWNVEVLTATQ 290
QY 297 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIEKTISKAKGQPREPQVYT 356
Db 291 THREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYV 350
QY 357 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKL 416
Db 351 LPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGYSFYMSKL 410
QY 417 TVDKSRWQOQGNVFCSCVMHEALHNHYTKSLSPG 452
Db 411 RVEKKNWVERNSYSCSVVHEGLHNHHTKSFSTRTPG 446

RESULT 12
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A02157; A26235; A26232; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi
A:Reference number: S25057
A:Accession: S25057
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827

Db 374 PQVYILSPPEQLSRKDVSLTCLAVGFSPEDISVEWTSNGHTEENYKDTAPVLDSDGSYF 433
QY 412 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 453
Db 434 IYSKLNMKTSKWEKTDSCNVRHEGLKNYILKKTISRSPGK 475

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124
C:Genetics:
A:Gene: IgG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 1263; DB 2; Length 328;
Best Local Similarity 70.3%; Pred. No. 1.7e-66;
Matches 230; Conservative 43; Mismatches 48; Indels 6; Gaps 2;

QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 188
Db 6 PSVYPLAPCSRDTSGPNVALGCLASSYFFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 65
QY 189 SSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFL 248
Db 66 SSMVTVPASSLSKSYTCNVNHPATTTTKVDKRVGKTKPPCPICPACESP----GPSVFI 121
QY 249 FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 308
Db 122 FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 181
QY 309 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ 368
Db 182 VSVLPVPIQHQQDWLNGKEYKCKVNNKDLPAITRIISKAKGQTPREPVYTLPPHAEELSRSK 241
QY 369 VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQQG 426
Db 242 VSITCLVIGFYPDPIDVEWQRNGQPEPEGNVYRTTPQQDVGDTYFLYSKFSVDKASWQQG 301
QY 427 NVFSCSVMEALHNHYTQKSLSLSPGK 453
Db 302 GIFQCVMHEALHNHYTQKSISKTPGK 328

RESULT 15
I47160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAA52218.1; PID:g433126
C:Genetics:

A:Gene: IgG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 51.7%; Score 1257; DB 2; Length 328;
Best Local Similarity 70.0%; Pred. No. 3.7e-66;
Matches 229; Conservative 42; Mismatches 50; Indels 6; Gaps 2;

QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 188
Db 6 PLVYPLAPCGRDTSGPNVALGCLASSYFFPEPTVSWNSGALTSGVHTFPAVLQSSGLYSL 65
QY 189 SSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFL 248
Db 66 SSMVTVPASSLSKSYTCNVNHPATTTTKVDKRVGKTKPPCPICPACESP----GPSVFI 121
QY 249 FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 308
Db 122 FPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 181
QY 309 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ 368
Db 182 VSVLPVPIQHQQDWLNGKEYKCKVNNKDLPAITRIISKAKGQTPREPVYTLPPHAEELSRSK 241
QY 369 VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDSDGSFFLYSLKLTVDKSRWQQG 426
Db 242 VSITCLVIGFYPDPIDVEWQRNGQPEPEGNVYRTTPQQDVGDTYFLYSKFSVDKASWQQG 301
QY 427 NVFSCSVMEALHNHYTQKSLSLSPGK 453
Db 302 GIFQCVMHEALHNHYTQKSISKTPGK 328

Search completed: August 12, 2003, 16:32:18
Job time : 21.2534 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:22:22 ; Search time 12.152 Seconds
(without alignments)
1753.051 Million cell updates/sec

Title: US-09-802-077-8
Perfect score: 2432
Sequence: 1 EVQLVESGGLVQPGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1750	72.0	330	1 GC1_HUMAN	P01857 homo sapien
2	1599	65.7	326	1 GC2_HUMAN	P01859 homo sapien
3	1585.5	65.2	327	1 GC4_HUMAN	P01861 homo sapien
4	1231.5	50.6	323	1 GC_RABIT	P01870 oryctolagus
5	1202.5	49.4	329	1 GC2_CAVPO	P01862 cavia porce
6	1162	47.8	290	1 GC3_HUMAN	P01860 homo sapien
7	1150	47.3	326	1 GC1_RAT	P20759 rattus norv
8	1142	47.0	324	1 GC1_MOUSE	P01868 mus musculu
9	1142	47.0	329	1 GC3_MOUSE	P22436 mus musculu
10	1139.5	46.9	333	1 GCB_RAT	P20761 rattus norv
11	1137	46.8	393	1 GC1M_MOUSE	P01869 mus musculu
12	1131	46.5	398	1 GC3M_MOUSE	P03987 mus musculu
13	1126	46.3	330	1 GCAA_MOUSE	P01863 mus musculu
14	1123.5	46.2	335	1 GCAB_MOUSE	P01864 mus musculu
15	1121	46.1	399	1 GCAM_MOUSE	P01865 mus musculu
16	1117.5	45.9	329	1 GCC_RAT	P20762 rattus norv
17	1110	45.6	322	1 GCA_RAT	P20760 rattus norv
18	1082	44.5	336	1 GCB_MOUSE	P01866 mus musculu
19	1077	44.3	405	1 GCBM_MOUSE	P01867 mus musculu
20	482.5	19.8	429	1 EPC_RAT	P01855 rattus norv
21	478	19.7	428	1 EPC_HUMAN	P01854 homo sapien
22	468	19.2	421	1 EPC_MOUSE	P06336 mus musculu
23	441	18.1	454	1 MUC_HUMAN	P01871 homo sapien
24	439.5	18.1	122	1 HV3G_HUMAN	P01768 homo sapien
25	437.5	18.0	458	1 MUC_RABIT	P03988 oryctolagus
26	431.5	17.7	455	1 MUC_MOUSE	P01872 mus musculu
27	427.5	17.6	479	1 MUCM_RABIT	P04221 oryctolagus
28	421.5	17.3	476	1 MUCM_MOUSE	P01873 mus musculu
29	421	17.3	119	1 HV3I_HUMAN	P01770 homo sapien
30	420	17.3	123	1 HV24_MOUSE	P01793 mus musculu
31	419	17.2	120	1 HV3E_HUMAN	P01766 homo sapien
32	418	17.2	457	1 MUC_SUNMU	P20768 suncus muri
33	415.5	17.1	114	1 HV3B_HUMAN	P01763 homo sapien

34	414	17.0	450	1 MUC_CANFA	P01874 canis famil
35	413.5	17.0	454	1 MUC_MESAU	P06337 mesocricetu
36	413	17.0	121	1 HV3J_HUMAN	P01771 homo sapien
37	412	16.9	115	1 HV3F_HUMAN	P01767 homo sapien
38	410	16.9	115	1 HV3D_HUMAN	P01765 homo sapien
39	406.5	16.7	116	1 HV05_CARAU	P19181 carassius a
40	405.5	16.7	122	1 HV3H_HUMAN	P01769 homo sapien
41	405	16.7	123	1 HV22_MOUSE	P01791 mus musculu
42	404.5	16.6	116	1 HV3T_HUMAN	P01781 homo sapien
43	403.5	16.6	120	1 HV3U_HUMAN	P01782 homo sapien
44	403	16.6	113	1 HV30_MOUSE	P01799 mus musculu
45	403	16.6	391	1 MUCB_HUMAN	P04220 homo sapien

ALIGNMENTS

RESULT 1
GCL_HUMAN
ID GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig.gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gammal gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]
RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=684994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.;
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -!- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE
CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)
CC MARKER & THE GLM (NON-1) MARKERS.
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A93433; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR PDB; 1AJ7; 12-NOV-97.
DR PDB; 1D5B; 09-FEB-00.
DR PDB; 1D5I; 09-FEB-00.
DR PDB; 1D6V; 04-OCT-00.
DR PDB; 1DN2; 17-MAY-00.
DR PDB; 1E4K; 06-JUN-01.
DR PDB; 1FCC; 20-JUL-95.
DR PDB; 1HZH; 12-JUN-02.
DR PDB; 1I7Z; 08-AUG-01.
DR PDB; 1IIS; 16-MAY-01.
DR PDB; 1IIX; 16-MAY-01.
DR PDB; 1L6X; 10-APR-02.
DR PDB; 2RCS; 12-NOV-97.
DR Genew; HGNC:5525; IGHG1.
DR MIM; 147100; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding activity; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.

FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT
FT VARIANT 239 239
FT
FT VARIANT 241 241
FT
FT STRAND 122 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 147
FT STRAND 157 162
FT TURN 163 164
FT STRAND 165 166
FT TURN 168 171
FT STRAND 176 179
FT TURN 180 181
FT STRAND 182 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 207
FT TURN 209 210
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 242
FT STRAND 245 256
FT STRAND 260 265
FT STRAND 270 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 305 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 325
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 72.0%; Score 1750; DB 1; Length 330;
Best Local Similarity 98.8%; Pred. No. 5.1e-113;
Matches 328; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 58

QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 241
Db 59 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 118

QY 242 GGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
Db 119 GGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 178

QY 302 YNSTYRVVSVLTVHLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 361
Db 179 YNSTYRVVSVLTVHLQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 238

QY 362 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 421
Db 239 DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 298

QY 422 RWQQGNVFCSCVMHEALHNHYTQKSLSPGK 453
Db 299 RWQQGNVFCSCVMHEALHNHYTQKSLSPGK 330

RESULT 2

GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RT heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
RT evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
RT evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
RT domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
RT immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=9525298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins.";

RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute Of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00230; AAB59393.1; -.
DR PIR; A93906; G2HU.
DR HSSP; P01857; 1FC1.
DR Genew; HGNC:5526; IGHG2.
DR MIM; 147110; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding activity; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CHI.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156 AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT MOD_RES 326 326 REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT VARIANT 60 60 S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT CONFLICT 109 109 /FTid=VAR_003889.
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
C -> S (IN REF. 3).
Query Match 65.7%; Score 1599; DB 1; Length 326;
Best Local Similarity 91.3%; Pred. No. 1.1e-102;
Matches 303; Conservative 10; Mismatches 13; Indels 6; Gaps 3;
QY 122 ASTKGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 58
QY 182 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELL 241
Db 59 SSGLYSLSSVVTVPSSNFGTQTYTCNVNDHKPSNTKVDKTKVERKCCVE--CPPCPAPP-V 114
QY 242 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
Db 115 AGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQ 174

```
QY 302 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPVYTLPPSR 361
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 175 FNSTERVSVLTVVHQDWLNGKEYCKVSNKGLPAPIEKTIISKTKGQPREPVYTLPPSR 234
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 421
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 235 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSGSFFLYSKLTVDKS 294
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 422 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 295 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 326
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
GC4_HUMAN
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Millstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; 1ADQ; 16-SEP-98.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding activity; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
```

```
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 65.2%; Score 1585.5; DB 1; Length 327;
Best Local Similarity 91.0%; Pred. No. 9.5e-102;
Matches 302; Conservative 10; Mismatches 15; Indels 5; Gaps 2;

QY 122 ASTKGKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
      ||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 AST--KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 58
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPCPAPELL 241
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 SSGLYSLSSVTVTPSSSLGTQTYTCNVNHNKPSNTKYDKRVESK---YGPCCPCPAPPEFL 115
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 242 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 301
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 116 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQ 175
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 302 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPSR 361
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 176 FNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPVYTLPPSQ 235
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 362 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 421
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 236 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 295
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 422 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 453
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 296 RWQEGNVFSCVMHEALHNHYTQKSLSLSPGK 327
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
GC_RABIT
ID GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
F-1 haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
immunoglobulin G.";
```



```
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almquist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
CC This SWISS-PROT entry is copyright.. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M16426; AAA31289.1; -.
DR PIR; A91749; GHRB.
DR HSSP; P01857; lFcl.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Repeat.
KW NON_TER 1 1
FT DOMAIN 1 6 96 IG-LIKE 1.
FT DOMAIN 114 213 IG-LIKE 2.
FT DOMAIN 222 318 IG-LIKE 3.
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 V -> VPV (IN REF. 2).
FT CONFLICT 71 71 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 144 144 N -> D (IN REF. 5).
FT CONFLICT 173 173 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 187 187 Q -> D (IN REF. 5).
FT CONFLICT 201 201 Q -> E (IN REF. 5).
FT CONFLICT 218 218 E -> Q (IN REF. 5).
FT CONFLICT 233 233 N -> D (IN REF. 5).
FT CONFLICT 246 246 E -> G (IN REF. 5).
FT CONFLICT 256 256 N -> D (IN REF. 5).
FT CONFLICT 260 260 Y -> W (IN REF. 5).
FT CONFLICT 266 266 N -> S (IN REF. 5).
FT CONFLICT 280 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 50.6%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 1.7e-77;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 127 KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLY 186
Db 4 KAPSVFPLAPCCGDTTPSSVTLGCLVKGYLPEPTVTWNSGTLTGVRTFSPVRSQSSGLY 63

QY 187 SLSSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHCTCPCPAPPELLGGPSV 246
Db 64 SLSSSVSVTSSS---QPVTCTNVAHPATNTKVDKTVAPSTCSK---PTCPPPELLGGPSV 116

QY 247 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 306
Db 117 FIFPPKPKDTLMISRTPEVTCVVVDVSDDDPEVQFTWYINNEQVTTARPPLREQQFNSTI 176

QY 307 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 366
Db 177 RVVSTPLPIHQDWLRGKEFKCKVHNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSS 236
```

```
QY 367 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 426
Db 237 RSVSLTCMINGFYPSDISVEWEKNGKAEDNYKTTPPAVLDSGDSYFLYNKLSVPTSEWQRG 296

QY 427 NVFSCSVMEALHNHYTQKSLSLSPGK 453
Db 297 DVFTCSVMHEALHNHYTQKSISRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
ID GC2_CAVPO
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A94553; G2GP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
```



```
FT VARIANT 126 127 QV -> EB (IN ZUC).
FT FTID=VAR_003890.
FT VARIANT 134 134 P -> L (IN OMM).
FT FTID=VAR_003891.
FT VARIANT 139 139 F -> Y (IN OMM).
FT FTID=VAR_003892.
FT VARIANT 182 182 T -> A (IN OMM).
FT FTID=VAR_003893.
FT VARIANT 227 227 S -> N (IN OMM).
FT FTID=VAR_003894.
FT VARIANT 227 227 MISSING (IN ZUC).
FT FTID=VAR_003895.
FT VARIANT 279 279 F -> Y (IN OMM).
FT FTID=VAR_003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;

Query Match 47.8%; Score 1162; DB 1; Length 290;
Best Local Similarity 91.4%; Pred. No. 8.8e-73;
Matches 212; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 222 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 281
Db 59 EPKSCDTPPPCPCRPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 118

QY 282 NWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKT 341
Db 119 KQYVDGVQVHNAKTPREQQFNSTFRVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKT 178

QY 342 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 401
Db 179 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238

QY 402 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCFSVMHEALHNHYTQKSLSLSPGK 453
Db 239 PMLDSGDSFFLYSKLTVDKSRWQQGNIFCSVMHEALHNRFQKSLSLSPGK 290
```

```
RESULT 7
GCL_RAT
ID GCL_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
```

```
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC....) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 47.3%; Score 1150; DB 1; Length 326;
Best Local Similarity 64.0%; Pred. No. 6.7e-72;
Matches 210; Conservative 51; Mismatches 57; Indels 10; Gaps 4;

QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 188
Db 6 PSVIPLAPGTALKSNMVTLGCLVKGYFPEPVTVWNSGALSSGVHTFPAVLQ-SGLYTL 64

QY 189 SSVTVPPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELGG--PS 245
Db 65 TSSVTVPPSSTWPSQTVCNVAHPASSTKVDKKIVPRNCG--GDCKPC---ICTGSEVSS 118

QY 246 VLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 305
Db 119 VFIFPPKPKDVLITITLTPKVTCTVVDISQDDPEVHFSWFDVDEVHTAQTRPPEEQFNST 178

QY 306 YRVVSVLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMT 365
Db 179 FRVSSELPILHQDLNGLNGRTFRCKVTSAAFPSPIEKTIKDEGRTQVPHVYTMSPTEEMT 238

QY 366 KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDKSRWQQ 425
Db 239 QNEVSITCMVKGFYPPDIYVWQMNGQPQENYKNTPTPTMDTDGSGYFLYSKLVNKKKWOQ 298

QY 426 GNVFSCSVMEALHNHYTOKSLSLSPGK 453
Db 299 GNTFTCSVLHEGLHNHHTKSLSHSPGK 326
```

```
RESULT 8
GCL_MOUSE
ID GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
RT cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
RT heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
```


Db 5 PSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ-SGFYSL 63

QY 189 SSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCP--PCPAPELLGGPSV 246

Db 64 SSVTVPSSTWPSQTVICNVNHAHPASKTELKRIEPR-IPKPSTPPGSSCPPGNILGGPSV 122

QY 247 FLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNSTY 306

Db 123 FIFPPKPKDALMISLTPKVTICNVVDVSEDDPDVHVSFWFVDNKEVHTAWTPREAQYNSTF 182

QY 307 RVVSVTLVLHQDLWNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 366

Db 183 RVVSALPIQHODWMRGKEFKCKVNKALPAPIERTISKPKGRAQTPQVYTIPTPPREQMSK 242

QY 367 NOVSLTCLVKGYFYPSPDIAEVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 426

Db 243 KKVSLTCLVNTFFSEAIISVEVERNGELEQDYKNTPIILDSGTIFYLYSKLTVDTDSDLQ 302

QY 427 NVFSCSVMHREALHNHYTQKSLSLSPGK 453

Db 303 EIFTCVVHREALHNHHTQKNLSRSPGK 329

RESULT 10

GCB_RAT

ID GCB_RAT STANDARD; PRT; 333 AA.

AC P20761;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig gamma-2B chain C region.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1].

RP SEQUENCE FROM N.A.

RX MEDLINE=89232738; PubMed=3149946;

RA Brueggemann M.;

RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";

RL Gene 74:473-482(1988).

CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

DR PIR; PS0018; PS0018.

DR HSSP; P01842; 7FAB.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Repeat.

FT NON_TER 1

FT DOMAIN 6 96 IG-LIKE 1.

FT DOMAIN 124 223 IG-LIKE 2.

FT DOMAIN 232 328 IG-LIKE 3.

FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 80

FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 147 207

FT DISULFID 253 311

SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 46.9%; Score 1139.5; DB 1; Length 333;

Best Local Similarity 64.4%; Pred. No. 3.6e-71;

Matches 213; Conservative 44; Mismatches 65; Indels 9; Gaps 3;

QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 188

||||| | : | ||||| ||||| : ||||| ||||| : ||||| |||||

Db 6 PSVYPLAPGCGDTSSTVTTLGCLVKGYFPEPVTVWNSGALSSDVHTFPAVLQ-SGLYTL 64

QY 189 SSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKS-----CDKTHTCPPCPAPELLG 242

Db 65 TSSVT--SSTWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCTCPTCHKCPVELLG 122

QY 243 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 302

Db 123 GPSVFIFPPPKPKDILLISQNAKVTCTVVVDVSEEDPDVQFSWFVNNVEVHTAQTQPREEQ 182

QY 303 NSTYRVVSVTLVLHQDLWNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 362

Db 183 NSTFRVVSALPIQHODWMSGKEFKCKVNKALPAPIEKTISKPKGLVRKPKQVYVMGPPE 242

QY 363 EMTKNQVSLTCLVKGYFYPSPDIAEVESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 422

Db 243 QLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTPEVMDSDGSFFMYSKLNVERSR 302

QY 423 WQOGNVFSCSVMHREALHNHYTQKSLSLSPGK 453

Db 303 WDSRAPEVCSVVHEGLHNHHVEKSISRPPGK 333

RESULT 11

GCLM_MOUSE

ID GCLM_MOUSE STANDARD; PRT; 393 AA.

AC P01869;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ig gamma-1 chain C region, membrane-bound form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1].

RP SEQUENCE FROM N.A.

RX MEDLINE=80045036; PubMed=115593;

RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.;

RT "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";

RT Cell 18:559-568(1979).

RN [2].

RP SEQUENCE OF 323-393 FROM N.A.

RX MEDLINE=82197626; PubMed=6804950;

RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;

RT "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular domain.";

RT Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).

RN [3].

RP SEQUENCE OF 323-366 FROM N.A.

RX MEDLINE=82115295; PubMed=6799207;

RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.;

RT "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";

RL Cell 26:19-27(1981).

RN [4].

RP SEQUENCE OF 1-44 FROM N.A.

RX MEDLINE=82222190; PubMed=6283537;

RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

RT "Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Membrane-bound;

CC IsoId=P01869-1; Sequence=Displayed;

CC Name=Secreted;

CC IsoId=P01868-1; Sequence=External;

CC Note=May be the major isoform;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; V00793; CAA24172.1; -
EMBL; V00793; CAA24173.1; -
EMBL; V00793; CAA24174.1; -
PIR; B02159; G1MSM.
PDB; 15C8; 23-MAR-99.
PDB; 1AE6; 18-MAR-98.
PDB; 1CL7; 12-JAN-00.
PDB; 1F11; 06-FEB-01.
PDB; 1F58; 29-DEC-99.
PDB; 1KC5; 24-JUL-02.
PDB; 1KCR; 11-MAY-02.
PDB; 25C8; 09-JUL-99.
MGD; MGI:96446; Igh-4.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGcl; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane; 3D-structure.
NON_TER 1 1
DOMAIN 1 97 CH1.
DOMAIN 98 110 HINGE.
DOMAIN 111 217 CH2.
DOMAIN 218 324 CH3.
DISULFID 27 82
DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 138 198
CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
DISULFID 244 302
TRANSMEM 340 357 POTENTIAL.
DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 46.8%; Score 1137; DB 1; Length 393;
Best Local Similarity 62.9%; Pred. NO. 6.6e-71;
Matches 205; Conservative 54; Mismatches 57; Indels 10; Gaps 4;

QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSSGLYSL 188
Db 6 PSVYPLAPGSAQTNSMVTLGCLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQSD-LYTL 64
QY 189 SSVVTPVSSSLGTQTYICNVNHKPSNTKVKDKKVEPKSCDKTHTCPP--CPAPELGGPSV 246
Db 65 SSVVTPVSSPRPSETVTCNVAHPASSTKVKDKKIVPRDCG----CKPCICTVPEV---SSV 117
QY 247 FLFPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNSIY 306
Db 118 FIFPPKPKDVLITLTLPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQNSTF 177
QY 307 RVVSVLTVLHQDLNGKEYCKCKVSKNKAIPAEKTIKAKGQPREPQVYTLPPSREEMTK 366
Db 178 RSVSELPIMHQDWLNGKEFKCRVNSAAFPAPAEKTIKTKGRPKAPQVYTIPTPPKEQMAK 237
QY 367 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQG 426
Db 238 DKVSLTCTMTDFPEDITVEWQWNGQPAENYKNTQPIMTNGSYFVYSKLVNPKNSWEAG 297
QY 427 NVFSCSVMEALHNHYTQKSLSLSPG 452

Db 298 NTFTCSVLHEGLHNHHTEKSLSHSPG 323
RESULT 12
GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00451; AAB59655.1; -
DR EMBL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A02156; G3MSM.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362 POTENTIAL.
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 46.5%; Score 1131; DB 1; Length 398;
Best Local Similarity 64.9%; Pred. NO. 1.7e-70;
Matches 211; Conservative 44; Mismatches 66; Indels 4; Gaps 3;

QY 129 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSVNSGALTSGVHTFPAVLQSSGLYSL 188
Db 5 PSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPTVKWNGALSSGVRTVSSVLQ-SGFYSL 63

QY 189 SSVTVFPSSSLGTQTYICNVNHHKPSNTKVDDKKVEPKSCDKTHTCP--PCPAPELLGGPSV 246
||:|||||: :|| |||| | ||: ||:|: | | | | | :|||||
Db 64 SSLTVFSSSTWPSQTVICNVVAHPASKTELIKRIEPR-IPKPSPPGSSCPPGNILGGPSV 122

QY 247 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 306
|:||||| |||| ||:||||| ||:| :|:| | | | | | | | | | |
Db 123 FIFPPKPKDALMISLTPKVTCTVVVDVSEDDPDVHVSWFVDNKEVHTAQTQPREAQYNSTF 182

QY 307 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK 366
|||| | : ||||: ||:||||:||||| ||:| | | | | : ||||:| | | | |
Db 183 RVVSALPIQHQQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPTPPREQMSK 242

QY 367 NQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 426
:||||| | : |||| | | : |||| | | : ||||:||||| | | |
Db 243 KKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTFLYSKLTVDTSWLQG 302

QY 427 NVFSCSVMHREALHNHYTQKSLSLSP 451
:||||:||||| ||:| | | | |
Db 303 EIFTCSVVHEALHNHHTQKNLSRSP 327

RESULT 13
GCAB_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollo R., Auffray C., Mochamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics' and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; 12-JUL-01.
DR PDB; 1E4X; 12-JUL-01.
DR PDB; 1MNU; 06-MAY-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
KW NON_TER 1 98
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 46.3%; Score 1126; DB 1; Length 330;
Best Local Similarity 64.0%; Pred. No. 3e-70;
Matches 212; Conservative 42; Mismatches 73; Indels 4; Gaps 3;

QY 125 KGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHFFPAVLQSSG 184
| : ||||| | : | : ||||| ||||| : ||||| ||||| |||||
Db 2 KTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPTLTWNSGSLSSGVHFFPAVLQSD- 60

QY 185 LYSLSVVTVFPSSSLGTQTYICNVNHHKPSNTKVDDKKVEPKSCDKTHTCP--CPAPELLG 242
||:|||| |||| | : | | | | | : ||||| : ||: ||||| |||||
Db 61 LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDDKKIEPRG-PTIKPCPPCKCPAPNLLG 119

QY 243 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 302
||||:|||| | |||| | ||||| ||||| : ||: | : |||| | : |
Db 120 GPSVFIFPPKIKDKVLMISSLPIVTCVVVDVSEDDPDVQISWFWNNVEVHTAQTQTHREDY 179
..
QY 303 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 362
||| |||| | : ||||:||||:||||:||||:||||:||||: || | |||| ||| |
Db 180 NSTLRVVSALPIQHQQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEE 239

QY 363 EMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 422
|||| ||:||||: | | | | | : ||: | | | | | ||||| : |||| | : |
Db 240 EMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTPEVLDSDGSYFMYSKLRVEKN 299
..
QY 423 WQQGNVFCSCVMHEALHNHYTQKSLSLSPCK 453
| : | : ||||: || ||||: || | | | | |
Db 300 WVERNSYSCSVVHEGLHNHHTTKFSRTPGK 330

RESULT 14
GCAB_MOUSE STANDARD; PRT; 335 AA.
ID GCAB_MOUSE
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).

FT	DISULFID	112	112	INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	TRANSMEM	346	363	POTENTIAL.
FT	DOMAIN	364	399	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	180	180	N-LINKED (GLCNAC...)(POTENTIAL).
SQ	SEQUENCE	399 AA;	44020 MW;	4C38138BFAED3FF0 CRC64;
Query Match 46.1%; Score 1121; DB 1; Length 399;				
Best Local Similarity 63.9%; Pred. No. 8.4e-70;				
Matches 211; Conservative 42; Mismatches 73; Indels 4; Gaps 3;				
QY	125	KGKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG	184	
Db	2	KTAPSVYPLAPVCGDTTGGSSVTLGCLVKGYFPEPVTLTWSGSLSSGVHTFPAVLQSD-	60	
QY	185	LYSLSSVWTVPSSSLGTQTYICNVNHNKPSNTKKVDKKVEPKSCDKTHTCPP--CPAPELLG	242	
Db	61	LYTLSSSVTVTSSWPSQSITCNVAHPASSTKKVDKKIEPRG-PTIKPCPPCKCPAPNLLG	119	
QY	243	GPSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY	302	
Db	120	GPSVFIFPPKIKDVLMLISLPIVTCVVVDVSEDDPDVQISWFEVNNVEVHTAQQTTHREDY	179	
QY	303	NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRE	362	
Db	180	NSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEE	239	
QY	363	EMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSR	422	
Db	240	EMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSGSGYFMYSKLRVEKN	299	
QY	423	WQOGNVFSCSVMHREALNHYTQKSLSLSPG	452	
Db	300	WVERNSYSCSVVHEGLHNHHTTKSFSTRTPG	329	

Search completed: August 12, 2003, 16:30:28
Job time : 14.152 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:24:12 ; Search time 45.2325 Seconds
(without alignments)
2584.378 Million cell updates/sec

Title: US-09-802-077-8
Perfect score: 2432
Sequence: 1 EVQLVESGGGLVQPGGSLRL.....MHEALHNHYTQKSLSLSPGK 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2201.5	90.5	471	4 Q8TC77	Q8tc77 homo sapien
2	2019.5	83.0	521	4 Q8N4Y9	Q8n4y9 homo sapien
3	1903	78.2	473	4 Q8TC63	Q8tc63 homo sapien
4	1611.5	66.3	509	4 Q8NF17	Q8nf17 homo sapien
5	1552.5	63.8	469	11 Q8R3V9	Q8r3v9 mus musculu
6	1511.5	62.2	437	11 Q9RIA4	Q9rla4 mus musculu
7	1469.5	60.4	463	11 Q99LC4	Q99lc4 mus musculu
8	1463.5	60.2	473	11 Q91Z05	Q91z05 mus musculu
9	1450.5	59.6	473	11 Q9D8L4	Q9d8l4 mus musculu
10	1424	58.6	468	11 Q99L31	Q99l31 mus musculu
11	1423.5	58.5	473	11 Q99L25	Q99l25 mus musculu
12	1371	56.4	474	11 Q8R3H6	Q8r3h6 mus musculu
13	1258	51.7	701	4 Q96P08	Q96pq8 homo sapien
14	1249.5	51.4	337	6 Q95M34	Q95m34 equus cabal
15	875.5	36.0	597	4 Q96BB9	Q96bb9 homo sapien
16	872	35.9	613	4 Q8WUK1	Q8wuk1 homo sapien

17	799.5	32.9	499	4 Q8N5K4	Q8n5k4 homo sapien
18	795	32.7	494	4 Q96K68	Q96k68 homo sapien
19	793.5	32.6	493	4 Q8NCL6	Q8ncl6 homo sapien
20	765.5	31.5	487	11 Q99KA4	Q99ka4 mus musculu
21	762	31.3	486	11 Q91Z07	Q91z07 mus musculu
22	759.5	31.2	597	4 Q9BU10	Q9bu10 homo sapien
23	757.5	31.1	614	4 Q96GA6	Q96ga6 homo sapien
24	753.5	31.0	597	4 Q9BQB8	Q9bqb8 homo sapien
25	750	30.8	613	4 Q96EY0	Q96ey0 homo sapien
26	749.5	30.8	588	4 Q8WUX4	Q8wux4 homo sapien
27	749.5	30.8	618	4 Q96AA6	Q96aa6 homo sapien
28	735.5	30.2	480	11 Q91XE1	Q91xe1 mus musculu
29	731.5	30.1	479	11 Q91WP5	Q91wp5 mus musculu
30	729	30.0	613	11 Q8VCX7	Q8vcx7 mus musculu
31	726	29.9	278	11 Q921K1	Q921k1 mus musculu
32	726	29.9	479	11 Q99M22	Q99m22 mus musculu
33	705	29.0	484	11 Q8VEA0	Q8vea0 mus musculu
34	688	28.3	496	4 Q96KX8	Q96kx8 homo sapien
35	679	27.9	496	4 Q96DK0	Q96dk0 homo sapien
36	674	27.7	482	11 Q91X92	Q91x92 mus musculu
37	671.5	27.6	497	4 Q8WY24	Q8wy24 homo sapien
38	666	27.4	488	11 Q91WR1	Q91wr1 mus musculu
39	664	27.3	500	4 Q9BRV0	Q9brv0 homo sapien
40	650	26.7	484	11 Q99LA6	Q99la6 mus musculu
41	649.5	26.7	481	11 Q91WT1	Q91wt1 mus musculu
42	644	26.5	573	4 Q8WU38	Q8wu38 homo sapien
43	640.5	26.3	481	11 Q8VCV5	Q8vcv5 mus musculu
44	632	26.0	416	4 Q9NPP6	Q9npp6 homo sapien
45	628	25.8	482	11 Q8K172	Q8k172 mus musculu

ALIGNMENTS

RESULT 1

Q8TC77					
ID	Q8TC77	PRELIMINARY;	PRT;	471 AA.	
AC	Q8TC77;				
DT	01-JUN-2002 (TREMBlrel. 21, Created)				
DT	01-JUN-2002 (TREMBlrel. 21, Last sequence update)				
DT	01-MAR-2003 (TREMBlrel. 23, Last annotation update)				
DE	Hypothetical protein.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Spleen;				
RA	Strausberg R.;				
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBDJ databases.				
DR	EMBL; BC024289; AAH24289.1; -				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; ig; 4.				
DR	SMART; SM00406; Igv; 1.				
DR	PROSITE; PS50835; IG_LIKE; 4.				
DR	PROSITE; PS00290; IG_MHC; 2.				
KW	Hypothetical protein.				
SQ	SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;				

Query Match 90.5%; Score 2201.5; DB 4; Length 471;
Best Local Similarity 91.6%; Pred. No. 6.3e-176;
Matches 417; Conservative 17; Mismatches 16; Indels 5; Gaps 4;

QY	1	EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGS-TN 59			
Db	20	EVQLVESGGGLVQPGGSLRLSCAAAGFTFSS-YSMNWVRQAPGKGLEWVSSMSSSSYYIY 78			
QY	60	YADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYF-GHWHFAVWGQGTLYT 118			
Db	79	YADSVKGRFTISRDNKNSLYLQMNSLRAEDTAVYYCARDRLQLTSYWFYFDLWGRGTLVT 138			

```
QY 119 VSSASTKGKPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 178
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 VSSAST--KGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 196
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 179 VLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAP 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 197 VLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAP 256
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 239 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 257 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 316
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 299 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP 358
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLP 376
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 359 PSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 418
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 436
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 419 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 437 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 2
Q8N4Y9 PRELIMINARY; PRT; 521 AA.
AC Q8N4Y9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells from Tonsils;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC033178; AAH33178.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;
```

```
Query Match 83.0%; Score 2019.5; DB 4; Length 521;
Best Local Similarity 77.2%; Pred. No. 1.3e-160;
Matches 390; Conservative 23; Mismatches 37; Indels 55; Gaps 5;
```

```
QY 1 EVQLVDSGGGLVQPGGSLRLSCAIVSGYSITSGYSWNWIRQAPGKLEWVA---SITYDGS 57
      |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 EVQLVDSGGGLVQPGGSLRLSCAASGFIVSDHYV-EWVRQAPGKGPWVGCFRSKAHKST 78
      |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 58 TNYADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFG--HWHFAYWGQGT 115
      || || ||||| ||||| |||||: |||||: ||||| ||||| ||||| ||||| |||||
Db 79 TEYAAVKGRFTILRDDSKNSVHLQMNSLKTDDTAVYYCVRDLEGAGCKYDWYFDIWRGI 138
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 116 LVTVSSASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 175
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 LVTVSSAST--KGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHT 196
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 176 FPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKV----- 221
```

```
Db 197 FPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVELKTPLGDTHTTCP 256
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 222 -----EPKSCDKTHTCPPCPAPPELLGGPSVFL 248
      ||||| || ||||| ||||| |||||
Db 257 RCPEPKSCDTPPPCPRCEPKKSCDTPPPCPRCEPKKSCDTPPPCPRCEPKKSCDTPPPCPR 316
      ||||| || ||||| ||||| |||||
QY 249 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV 308
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQFNSTFRV 376
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 309 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQ 368
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSREEMTKNQ 436
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 369 VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV 428
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 437 VSLTCLVKGFYPSDIAVEWESSGQPENNYTTPPMLDSGDSFFLYSKLTVDKSRWQQGNI 496
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 429 FSCSVMHEALHNHYTQKSLSLSPGK 453
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 497 FSCSVMHEALHNRFQKSLSLSPGK 521
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
RESULT 3
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
```

```
Query Match 78.2%; Score 1903; DB 4; Length 473;
Best Local Similarity 80.4%; Pred. No. 6.4e-151;
Matches 364; Conservative 33; Mismatches 48; Indels 8; Gaps 4;
```

```
QY 2 VQLVESGGGLVQPGGSLRLSCAIVSGYSI-TSGYSWNWIRQAPGKLEWVASITYDGSINY 60
      :|| ||| ||||| :|| ||| ||||| :|| ||| ||||| :|| ||| ||||| :|| |||
Db 28 LQLQESGPGLLKPSVTLSLTCTVSGDSVASSSYWGVRQPPGKLEWIGTINFGNMY 87
      :|| ||| ||||| :|| ||| ||||| :|| ||| ||||| :|| ||| ||||| :|| |||
QY 61 ADSVKGRFTISRDDSKNTFYLQMNSLRAEDTAVYYCARGSHYFGHWHFAYWGQGLTVTVS 120
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 88 SPSLRSRVMTSADMSSENSEPYLKLDSVTAADTAVYYCAAGHLVMFGF--AHWGQGLVSVS 145
      :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
QY 121 SASTKGKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180
      ||| ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146 PAST--KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 203
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 QSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVESK---YGPCCPCPAPEF 260
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


Qy	241	LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE	300
Db	261	LGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREE	320
Qy	301	QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPS	360
		:	
Db	321	QFNSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTISKAKGQPREPQVYITLPPS	380
Qy	361	REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK	420
		:	
Db	381	QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK	440
Qy	421	SRWQOGNVFSCSMHEALHNHYTQKSLSLSPGK	453
		:	
Db	441	SRWQEGNVFSCSMHEALHNHYTQKSLSLSLGK	473

RESULT	4
Q8NF17	
ID	Q8NF17
AC	PRELIMINARY; PRT; 509 AA.
DT	01-OCT-2002 (TReMBLrel. 22, Created)
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE	FLJ00385 protein (Fragment).
GN	FLJ00385.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-Spleen;
RA	Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RT	"The nucleotide sequence of a long cDNA clone isolated from human spleen.";
RL	Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AK090464; BAC03445.1; -.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig_cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PF00047; ig; 3.
DR	SMART; SM00407; IGcl; 3.
DR	PROSITE; PS50835; IG_LIKE; 3.
DR	PROSITE; PS00290; IG_MHC; 2.
FT	NON_TER 1
SQ	SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;

QY	374	LVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFELYSKLTVDKSRWQQGNVFSCSV	433
Db	361	LVKGFYPSDIAVWESSGQPENNYNTTPMLDSDGSFELYSKLTVDKSRWQQGNIFSCSV	420
QY	434	MHEALHNHYTQKSLSLSP	451
Db	421	MHEALHNRETQKSLSLSP	438

RESULT 5

Q8R3V9	ID	Q8R3V9	PRELIMINARY;	PRT;	469	AA.
AC		Q8R3V9;				
DT		01-JUN-2002 (TrEMBLrel. 21, Created)				
DT		01-JUN-2002 (TrEMBLrel. 21, Last sequence update)				
DT		01-MAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE		Hypothetical 52.0 kDa protein.				
OS		Mus musculus (Mouse).				
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX		NCBI_TaxID=10090;				
RN		[1]				
RP		SEQUENCE FROM N.A.				
RA		Strausberg R.;				
RL		Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR		EMBL; BC024405; AAH24405.1; -.				
DR		InterPro; IPR007110; Ig-like.				
DR		InterPro; IPR003006; Ig_MHC.				
DR		InterPro; IPR003596; Ig_v.				
DR		Pfam; PF00047; Ig; 4.				
DR		SMART; SM00406; IGV; 1.				
DR		PROSITE; PS50835; IG_LIKE; 4.				
DR		PROSITE; PS00290; IG_MHC; 1.				
KW		Hypothetical protein.				
SQ		SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;				

Query Match	63.8%;	Score 1552.5;	DB 11;	Length 469;
Best Local Similarity	63.3%;	Pred. No. 1.5e-121;		
Matches 292;	Conservative 66;	Mismatches 84;	Indels 19;	Gaps 8
QY 1	EVQLVESGGGLVQPGGSLRLSCA	VSGYSITSGYSWNWIRAPGKGL	EWVASITYDG---	S 57
	II IIIIIIIIIIIIIIIIIIIII	II:: I I:: I:: I:: I:: I::	I	:
DB 20	EVNLVESGGGLVQPGGSLRLSCA	ASGFTFD-YMSWVRPPGKALEWL	GFIRNKANGYT	78
QY 58	TNYADSVKGRFTISRDDSKNTFY	LQMNSLRAEDTAVYYCA--	RGSHYFGHWHF	AVWGQ 114
	I I:: IIIIIIIIIIIIIIIIIII	I:: I:: I:: I:: I:: I::	I I:: I:: I:: I::	
DB 79	TEYSASVKGRFTISRDNQSILYL	QMNALRAEDSATYYICARDRRSS	YYSGTSFAYWGQ	138
QY 115	TLVTSSASTKKGPSVFPPLAPSS	KSSTSGGTAALGCLVKDYFPEP	PTVTSWNSGALTS	GVH 174
	IIIII:: I IIIIIIIII I :	IIIII IIIIIIIIIIIIIIIII	IIIIIIIIIIIIIIII	
DB 139	TLVTSAAKT--TPPSVYPLAPGSA	AQTNSMVTGLCLVKGYFPEPTV	TWNSGSLSSGVH	196
QY 175	TFPAVLQSSGLYSLSSVTVTPSS	SLGTQTYICNVNHKPSNTKVDK	KVPEKSCDKTHT	CPP 234
	IIIIIII I:: IIIIIIIIIII::	II III I I:: I:: I:: I:: I::	I I I I:: I:: I I	
DB 197	TFPAVLQSD-LYTLSSVTVPSST	WPSQTVCNVAHPASSTKVDK	KIVPRDCG---	CKP 251
QY 235	--CPAPELLGGPSVFLFPPKPKD	TLMI	SRTPEVTCVVVDVSHEDPEVK	FNWYVDGVEVHN 292
	I II:: IIIIIIIIIII I I::	IIIIIIIIII:: I:: I:: I:: I::	I:: I:: I:: I:: I::	
DB 252	CICTVPEV---SSVFIFPPKPKD	VLITLT	PKVTCVVVDISKDDPEVQFS	WFVDDVEVHT 308
QY 293	AKTKPREEQYNSTYRVVSVLT	TVLHQDWLNGKEYKCKVSNKAL	PAPIEKTISKAKGQ	PREP 352
	I:: IIIIIIIIIII:: I I::	IIIIIIIIII:: I:: I:: I:: I::	I:: I:: I:: I:: I::	
DB 309	AQTKPREEQFNSTFRSVSELP	IMHQDWLNGKEFKCRVNSA	AFPAPIEKTISKTKGR	PKAP 368
QY 353	QVYTLPPSREEMTKNQVSLTCL	VKGYFPSDIAVEWESNGQPEN	NYKTTTPVLDSDGS	FFL 412
	IIIII:: I:: I:: IIIIIIIII::	I:: I:: I:: I:: I:: I::	I:: I:: I:: I:: I::	
DB 369	QVYTIPTPPKEQMAKDVKSLT	CMITDFFPEDITVEQWNGQ	PAENYKNTQPIMDT	DGSYFV 428
QY 413	YSKLTVDKSRWQQGNVFSCSVM	HEALHNHYTQKSLSLSPGK	453	
	IIII I I:: I I:: I:: I::	I:: I:: I:: I:: I:: I::		
DB 429	YSKLNQKSNWEAGNTFTCSVL	VEGLHNHHTKESLSHSPGK	469	

```
RESULT 6
Q9RIA4
ID Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Gammal heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scfv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh_v.
DR Pfam; PF00047; Igh; 4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match
Best Local Similarity 62.2%; Score 1511.5; DB 11; Length 437;
Matches 282; Conservative 70; Mismatches 83; Indels 19; Gaps 7;

QY 2 VQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNWIRQAPGKGLEWVASITYDGSNYA 61
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 VQLQESGGGLVQPGGSLKLSAASGFTFSS-YAMSWVRQTPKRLIEWVASFSSGGIYYT 59
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 DSVKGRFTISRDDSKNTFYIQLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTSS 121
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 DSVKGRFTIYKDKRNILSLQMSLSRSEDATAMYYCARGD-----YSAYWGPGILTVTSA 113
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 ASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 181
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 114 AKT--TPPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQ 171
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 SSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCTPP--CPAPE 239
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 172 SD-LYTLSSSVTVPPSSWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPE 226
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 LLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 299
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 227 V---SSVFIKPKPKDVLITITLTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPRE 283
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 EQYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP 359
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 284 EQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKGRPKAPQVYTIPP 343
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 SREEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVD 419
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 344 PKEQMAKDKVSLTCLVHEDLNHHTKNSLSPGK 437
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 420 KSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 404 KSNWEAGNTFTCSVLHEGLHNHTKNSLSPGK 437
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q99LC4
ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to RIKEN cDNA 1810060O09 gene.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh_v.
DR Pfam; PF00047; Igh; 4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBBC30783 CRC64;

Query Match
Best Local Similarity 60.4%; Score 1469.5; DB 11; Length 463;
Matches 274; Conservative 77; Mismatches 89; Indels 17; Gaps 9;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSWNWIRQAPGKGLEWVASITYDGSIN- 59
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 20 QVQLQQSGAELARPGASVRLSCKASGYTFT-GYGVSWVKQRTQGQLEWVGEI-YPGSGNT 77
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 -YADSVKGRFTISRDDSKNTFYIQLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVT 118
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 78 YYSEKFKGKATLTDTKSSSTAYMHLSSLTSEDSAVYFCARSS-YYSYDLFAYWGQGLTVT 136
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 VSSASTKGKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 178
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 137 VSAAKT--TPPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTFPA 194
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 VLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKKVEPKSCDKTHTCTPP--CP 236
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 195 VLQSD-LYTLSSSVTVPPSSWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICT 249
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 237 APELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 296
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 250 VPEV---SSVFIKPKPKDVLITITLTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQ 306
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 297 PREEQYNSTYRVVSVLTVQLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYT 356
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 307 PREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKGRPKAPQVYT 366
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 357 LPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKL 416
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 367 IPPPKEQMAKDKVSLTCLVHEDLNHHTKNSLSPGK 453
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 417 TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 453
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 427 NVQKSNWEAGNTFTCSVLHEGLHNHTKNSLSPGK 463
Dd :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q91Z05
ID Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 51.9 kDa protein.
GN AU044919.
```


RL .Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199:105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; Ig_c1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFDIF6 CRC64;

Query Match 51.4%; Score 1249.5; DB 6; Length 337;
Best Local Similarity 68.2%; Pred. No. 2.2e-96;
Matches 232; Conservative 45; Mismatches 52; Indels 11; Gaps 4;

QY 122 ASTKKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 181
Db 1 AST--TAPKVFALAPCGGTSDSTVALGCLVSGYFPEPVKVSWSGSLTSGVHTFPSVLQ 58

QY 182 SSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEP-----KSCDKTHTCPPC 235
Db 59 SSGFYSLSSMTVPASTWTSETYICNVVHAASNPKVDKRIEPIPDNHQKVCNDS-KCPKC 117

QY 236 PAPELLGGPSVFLPCKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 295
Db 118 PAPELLGGPSVFIFFPNPKDTLMITRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 177

QY 296 KPREEQNSTYRVSVSLVTLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 355
Db 178 RPKEEQNSTYRVSVSLVRLIQHDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 237

QY 356 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLY 413
Db 238 VLAPHPDELSSKSVSVTCLVKDFYPPEINIEWQSNQGOPELETIKYSTTQAQQSDGSFYLY 297

QY 414 SKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 298 SKLSVDRNRWQGTFTTCGMHEALHNHYTQKNVSKNPGK 337

RESULT 15
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (Oct-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC015760; AAH15760.1; -;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.

DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 36.0%; Score 875.5; DB 4; Length 597;
Best Local Similarity 36.7%; Pred. No. 1.1e-64;
Matches 208; Conservative 81; Mismatches 158; Indels 119; Gaps 20;

QY 1 EVQLVESGGGLVQPGGSLRLSCAVSIGYSITSGYSWNWIRQAPGKGLEWVASIT-YDGSIN 59
Db 20 EVQLLESGGGLVQPGGSLRLSCAASGFSFSS-YAMNWVRQAPGKGLEWVSAISGSGSTY 78

QY 60 YADSVKGRFTISRDDSKNTFYLQMNLSRAEDTAVYYCA---RGSHYFGHW-HFAVWGQGT 115
Db 79 YADSVKGRFTISRDNSTRDTLYLQMNLSRAEDTAVYYCAKDPGRYSASGNYTREYWGQGT 138

QY 116 LVTVSSASTKKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSG 172
Db 139 LVTVSSGS--ASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISS 196

QY 173 VHTFPAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNHNKPSN-----T 215
Db 197 TRGFPSVLR-GGKYAATSQVLLPSKDVMOGTDEHVVCKVQHPNGNKEKNVPLPVIAELPP 255

QY 216 KVDKKVEPKS-----CDKTHTCP-----VFLFPPKP 253
Db 256 KVSFVPPRDGFFGNPRKSKLICQATGFSRQIQVSWLREGKQVSGVTTDQVQAEAKES 315

QY 243 GPS-----VFLFPPKP 253
Db 316 GPITYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQONASSMCVDPDQDTAIRVPAIPPS- 374

QY 254 KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT 313
Db 375 FASIFLTKSTKLTCLVTDLTYYD-SVTISWTRQNGEAVKTHTNISESHPNATFSAVGEAS 433

QY 314 VLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQF-REPQVYTLPPSREEMT-KNQVSL 371
Db 434 ICEDDWNSEGERFTCTVHTDLPSPKQTSIRPKGVALHRPDPVYLLPPAREQLNRESATI 493

QY 372 TCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKLTVDKSRWQGN 427
Db 494 TCLVTGFSPADVFVQWNRGQPLSPEKYVTSADMPPEPQAGRYFAHSILTVSEEWNTGE 553

QY 428 VFSCSVMHEALHNHYTQKSLSLSPGK 453
Db 554 TYTCVVAHEALPNRVTERTVDKSTGK 579

Search completed: August 12, 2003, 16:31:42
Job time : 47.2325 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:17:47 ; Search time 25.6662 Seconds
(without alignments)
1348.171 Million cell updates/sec

Title: US-09-802-077-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLASVGDVRT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1135	100.0	218	20	AAW95658
2	1135	100.0	218	21	AAW85200
3	1135	100.0	218	22	AAB76947
4	1128	99.4	218	14	AAR33312
5	1112	98.0	218	20	AAW50030
6	1112	98.0	218	20	AAW95660
7	1112	98.0	218	20	AAW95662
8	1112	98.0	218	21	AAB07472
9	1112	98.0	218	22	AAB74211

10	1109	97.7	218	20	AAW95669	Mus musculus anti-
11	1109	97.7	218	20	AAW95664	Mus musculus anti-
12	1109	97.7	218	22	AAB47087	Anti-IgE antibody,
13	1109	97.7	218	22	AAB76949	Full length light
14	1109	97.7	218	22	AAB76951	Full length light
15	1109	97.7	218	22	AAB76953	Variable light cha
16	1109	97.7	218	22	AAB76958	Variable light cha
17	1108	97.6	218	18	AAW13563	Humanised anti-L-s
18	1100	96.9	238	21	AAW90930	Humanised anti-Fas
19	1100	96.9	238	23	ABB74899	Humanised anti-Fas
20	1099	96.8	238	21	AAW90932	Humanised anti-Fas
21	1099	96.8	238	23	ABB74901	Humanised anti-Fas
22	1096	96.6	238	21	AAW90931	Humanised anti-Fas
23	1096	96.6	238	23	ABB74900	Humanised anti-Fas
24	1036	91.3	214	21	AA93735	The kappa chain of
25	1036	91.3	238	19	AAW83034	Anti-Fas humanised
26	1036	91.3	238	21	AAB14777	Humanised anti-Fas
27	1036	91.3	238	21	AAW90927	Humanised HFE7A de
28	1036	91.3	238	23	ABB74896	Humanised anti-Fas
29	1036	91.3	238	23	ABB74942	Humanised anti-Fas
30	1031.5	90.9	237	21	AA96298	Human IGFAM-10 imm
31	1031	90.8	238	19	AAW83031	Anti-Fas humanised
32	1031	90.8	238	21	AAB14772	Humanised anti-Fas
33	1031	90.8	238	21	AAW90922	Humanised anti-Fas
34	1031	90.8	238	23	ABB74891	Humanised anti-Fas
35	1031	90.8	238	23	ABB74937	Humanised anti-Fas
36	1028	90.6	240	24	ABJ38594	Hepatitis C virus
37	1027.5	90.5	237	21	AA96289	Human IGFAM-1 immu
38	1026	90.4	260	23	ABP41164	Human ovarian anti
39	1024	90.2	240	24	ABJ38595	Hepatitis C virus
40	1019.5	89.8	237	21	AA96301	Human IGFAM-13 imm
41	1018	89.7	238	19	AAW83032	Anti-Fas humanised
42	1018	89.7	238	21	AAB14773	Humanised anti-Fas
43	1018	89.7	238	21	AAW90923	Humanised anti-Fas
44	1018	89.7	238	23	ABB74892	Humanised anti-Fas
45	1018	89.7	238	23	ABB74938	Humanised anti-Fas

ALIGNMENTS

RESULT 1	
AAW95658	
ID	AAW95658 standard; protein; 218 AA.
XX	
AC	AAW95658;
XX	
DT	08-JUN-1999 (first entry)
XX	
DE	Mus musculus anti-IgE e25 full length variable light chain.
XX	
KW	Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
KW	histamine; production; hypersensitivity; allergen; anaphylaxis;
KW	atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW	eczema; anaphylactic shock; urticaria.
XX	
OS	Mus musculus.
XX	
PN	WO9901556-A2.
XX	
PD	14-JAN-1999.
XX	
PF	30-JUN-1998; 98WO-US13410.
XX	
PR	02-JUL-1997; 97US-0887352.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Jardieu PM, Lowe J, Lowman HB, Presta LG;
XX	
DR	WPI; 1999-106057/09.
XX	
PT	Improving affinity of polypeptides, particularly anti-IgE antibodies

- by identifying aspartyl residues which undergo isomerisation and substituting alternative residues and screening for affinity against the target

Disclosure; Pages 91-92; 129pp; English.

The sequence is that of the full length variable light chain of e25. It was used as part of a method to improve the affinity of anti-IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be used for reducing or preventing IgE mediated production of histamine in a mammal. They can be used for treating a disorder mediated by IgE such as hypersensitivity, atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The antibodies can also be used for affinity purification, detection and diagnosis.

Sequence 218 AA;

Query Match 100.0%; Score 1135; DB 20; Length 218;
 Best Local Similarity 100.0%; Pred. No. 3.1e-57;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRVTITCRASQSVYDGD SYMNWYQKPGKAPKLLIYAASYLES 60
 |||||
 Db 1 DIQLTQSPSSLSASVGDRVTITCRASQSVYDGD SYMNWYQKPGKAPKLLIYAASYLES 60

QY 61 GVPSRFSGSGSDFTLTISSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120
 |||||
 Db 61 GVPSRFSGSGSDFTLTISSLQPEDFATYYCQOSHEDPYTFGGTKVEIKRTVAAPSVF 120

QY 121 IFPPSDEQLKSGTASVVCVLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
 |||||
 Db 121 IFPPSDEQLKSGTASVVCVLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
 |||||
 Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 2
 AAY85200

ID AAY85200 standard; protein; 218 AA.

XX
 AC AAY85200;

XX
 DT 29-JUN-2000 (first entry)

XX
 DE Light chain amino acid sequence of the humanised MaE11 antibody.

XX
 KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCEH;
 KW low affinity binding receptor; high affinity binding receptor; allergy;
 KW diagnosis; treatment; histamine release; light chain; prevent; chimeric.

XX
 OS Mus sp.

OS Homo sapiens.

XX
 PN US6037453-A.

XX
 PD 14-MAR-2000.

XX
 PF -06-JUN-1995; 95US-0466151.

XX
 PR 15-MAR-1995; 95US-0405617.

PR 14-AUG-1992; 92WO-US06860.

PR 26-JAN-1994; 94US-0185899.

XX
 PA (GETH) GENENTECH INC.

XX
 PI Presta LG, Jardieu PM;

XX
 DR WPI; 2000-269913/23.

XX
 PT New bispecific antibodies, useful for treating immunoglobulin

DR WPI; 2001-122353/13.
XX
PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display
XX
XX
PS Disclosure; Fig 2; 87pp; English.
XX
CC This invention relates to a nucleotide sequence encoding an antibody
CC with improved anti-IgE antibody activity. The antibody has improved
CC action due to a process comprising, a) identifying aspartyl residues
CC prone to isomerisation in unimproved anti-IgE (immunoglobulin E)
CC antibody; b) substituting alternative residues to create candidate
CC molecules, and c) selecting those candidate molecules which display
CC affinity against the target molecule. Use of the antibody results in
CC antiasthmatic; antiallergic; ophthalmological; dermatological and
CC antiinflammatory activity. The antibodies are useful for treating
CC IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis,
CC eczema, urticaria and food allergies. The mutant antibodies produced by
CC the above mentioned nucleic acids may also be used as affinity
CC purification agents and in diagnostic assays for detecting the expression
CC of an antigen of interest in specific cell, tissues or serum. Amino acid
CC sequences AAB76936-AAB76960 represent fragments of anti-IgE antibodies of
CC the invention. Polynucleotide sequence AAF69253 represents an expression
CC plasmid used in the course of the invention, and oligonucleotides
CC AAF69254 - AAF69271 are used in the generation of affinity improved
CC anti-IgE antibodies.
XX
SQ Sequence 218 AA;

Query Match 100.0%; Score 1135; DB 22; Length 218;
Best Local Similarity 100.0%; Pred. No. 3.1e-57;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTTITCRASQSVDYDGD SYMNNWYQKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSVDYDGD SYMNNWYQKPGKAPKLLIYAASYLES 60

Qy 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180

Qy 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4
AAR33312
ID AAR33312 standard; Protein; 218 AA.
XX
AC AAR33312;
XX
DT 25-MAR-2003 (updated)
DT 05-JUL-1993 (first entry)
XX
DE Humanised MaE11 Version 1 (intact IgG) light chain.
XX
KW Antibody; high affinity; FCEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; Fab; humael1v1.
XX
OS Synthetic.
XX
PN WO9304173-A1.
XX
PD 04-MAR-1993.
XX

PF 14-AUG-1992; 92WO-US06860.
XX
PR 14-AUG-1991; 91US-0744768.
PR 07-MAY-1992; 92US-0879495.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta LG;
XX
XX WPI; 1993-094004/11.
DR
XX Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
XX
PS Example 4; Fig 3; 113pp; English.
XX
CC Residues were selected from MaE11 and inserted or substituted into
CC a human Fab antibody background (Vh region Kabat subgroup III and V1
CC region kappa subgroup I). A first version, humael1v1 or version 1 is
CC given below. The affinity of version 1 was assayed and found to be
CC ca. 100 times lower than that of the donor antibody MaE11.
CC Therefore, further modifications in the sequence of version 1
CC were made.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 218 AA;

Query Match 99.4%; Score 1128; DB 14; Length 218;
Best Local Similarity 99.5%; Pred. No. 7.7e-57;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRTTITCRASQSVDYDGD SYMNNWYQKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTTITCRASQSVDYDGD SYMNNWYQKPGKAPKLLIYAASYLES 60

Qy 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120

Qy 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180

Qy 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5
AAY50030
ID AAY50030 standard; protein; 218 AA.
XX
AC AAY50030;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human E27 anti-IgE antibody light chain.
XX
KW Immunoglobulin E; IgE; antibody; vascular endothelial growth factor;
KW VEGF; chimeric; IgG; assay; FC gamma receptor; low affinity; hexamer;
KW complex; cross-linked; enzyme-linked immunosorbent assay; ELISA;
KW light chain.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9951642-A1.
XX
PD 14-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US06858.
XX

Pd	14-JAN-1999.
Xx	
Pf	30-JUN-1998; 98WO-US13410.
Xx	
Pf	02-JUL-1997; 97US-0887352.
Xx	(GETH) GENENTECH INC.
Pa	Jardieu PM, Lowe J, Lowman HB, Presta LG;
Xx	
Pi	WPI; 1999-106057/09.
Xx	
Dn	Improving affinity of polypeptides, particularly anti-IgE antibodies
Xx	- by identifying aspartyl residues which undergo isomerisation and
Pt	substituting alternative residues and screening for affinity against
Pt	the target
Xx	
Pt	Disclosure; Page 97; 129pp; English.
Xx	
Cc	The sequence is that of the full length heavy chain of e27. It
Cc	was used as part of a method to improve the affinity of anti-IgE
Cc	antibodies such as e26 and e27. The e26 and e27 antibodies can
Cc	be used for reducing or preventing IgE mediated production of
Cc	histamine in a mammal. They can be used for treating a disorder
Cc	mediated by IgE such as hypersensitivity, atopic allergy, asthma,
Cc	allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic
Cc	shock and urticaria. The antibodies can also be used for affinity
Cc	purification, detection and diagnosis.
Xx	
Sq	Sequence 218 AA;
	Query Match 98.0%; Score 1112; DB 20; Length 218;
	Best Local Similarity 98.2%; Pred. NO. 6.2e-56;
	Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy	1 DIQLTQSPSLASVSGDRVTITCRASQSVDYDGDSYMWNYYQQKPGKAPKLLIYAASYLES 60
Db	1 DIQLTQSPSLASVSGDRVTITCRASKPVDGEGDSYMWNYYQQKPGKAPKLLIYAASYLES 60
Qy	61 GVPSRFSCSGTGDTLTITSSLPEDFATYYCQSHSDPYTFQGTVKVEIKRTVAAPSVF 120
Db	61 GVPSRFSCSGTGDTLTITSSLPEDFATYYCQSHSDPYTFQGTVKVEIKRTVAAPSVF 120
Qy	121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLS 180
Db	121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSTYSLS 180
Qy	181 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
Db	181 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218
	RESULT 8
	AAB07472
ID	AAB07472 standard; protein; 218 AA.
Xx	
Ac	AAB07472;
Xx	
Dt	20-OCT-2000 (first entry)
Xx	
Xx	Amino acid sequence of E27 and anti-IgE antibody light chain.
De	
Xx	anti-IgE antibody; light chain; FC region; effector function; cancer;
Kw	allergy; asthma; LFA-1-mediated disorder; tumour; cancer.
Kw	
Xx	Synthetic.
Os	
Xx	
Pn	WO200042072-A2.
Xx	
Pd	20-JUL-2000.
Xx	
Pf	14-JAN-2000; 2000WO-US00973.
Xx	

PF 31-MAR-1999; 99US-0282505.
XX
PR 02-APR-1998; 98US-0080447.
XX
XX (GETH) GENENTECH INC.
PA
XX Idusogie EE, Presta LG, Mulkerrin MG;
PI
XX WPI; 2001-217935/22.
DR
XX
XX Novel polypeptide variant useful for treating cancers, allergic
PT diseases such as asthma and autoimmune diseases, comprises human
PT immunoglobulin-G Fc region, retains the ability to bind antigen and
PT does not activate complement
XX
XX Disclosure; Fig 4; 30pp; English.
PS
XX
XX The present invention relates to a variant of an antibody
CC having a human immunoglobulin (Ig)G Fc region, with an
CC amino acid substitution. The mutant retains the ability to
CC bind antigen. The invention is useful for determining the
CC presence of a protein of interest, by exposing the sample
CC suspected of containing the protein to the antibody and
CC determining the binding of it to the sample. The antibody
CC is also useful for treating cancer, allergic conditions
CC including asthma, LFA-mediated disorders, autoimmune
CC disorders and vasculitis.
XX
SQ Sequence 218 AA;
Query Match 98.0%; Score 1112; DB 22; Length 218;
Best Local Similarity 98.2%; Pred. No. 6.2e-56;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITICRASQSDYDGD SYMWNVYQQKPGKAPKLLIYAASYLE 60
Db
1 DIQLTQSPSSLSASVGDVRTITICRASQSDYDGD SYMWNVYQQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGGTDFTLTITISLQPEDFATYYCQQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGGTDFTLTITISLQPEDFATYYCQQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10
AAW95669
ID AAW95669 standard; protein; 218 AA.
XX
AC AAW95669;
XX
DT 08-JUN-1999 (first entry)
XX
DE Mus musculus anti-IgE e26 & e27 variable light chain F(ab)'2fragment.
XX
KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
KW histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; hypersensitivity; allergen; anaphylaxis;
KW eczema; allergic rhinitis; conjunctivitis; hay fever;
XX
OS Mus musculus.
XX
PN WO9901556-A2.
XX
PD 14-JAN-1999.
XX
PF 30-JUN-1998; 98WO-US13410.

XX 02-JUL-1997; 97US-0887352.
PR
XX (GETH) GENENTECH INC.
PA
XX
PI Jardieu PM, Lowe J, Lowman HB, Presta LG;
XX
DR WPI; 1999-106057/09.
XX
XX Improving affinity of polypeptides, particularly anti-IgE antibodies
PT - by identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against
PT the target
XX
PS Disclosure; Page 104; 129pp; English.
XX
XX The sequence is that of the variable light chain F(ab)'2 fragment of e26
CC and e27. It was used as part of a method to improve the affinity of
CC anti-IgE antibodies such as e26 and e27. The e26 and e27 antibodies can
CC be used for reducing or preventing IgE mediated production of
CC histamine in a mammal. They can be used for treating a disorder
CC mediated by IgE such as hypersensitivity, atopic allergy, asthma,
CC allergic rhinitis, conjunctivitis, hay fever, eczema, anaphylactic
CC shock and urticaria. The antibodies can also be used for affinity
CC purification, detection and diagnosis.
XX
SQ Sequence 218 AA;
Query Match 97.7%; Score 1109; DB 20; Length 218;
Best Local Similarity 97.7%; Pred. No. 9.2e-56;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITICRASQSDYDGD SYMWNVYQQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDVRTITICRASQSDYDGD SYMWNVYQQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGGTDFTLTITISLQPEDFATYYCQQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGGTDFTLTITISLQPEDFATYYCQQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 11
AAW95664
ID AAW95664 standard; protein; 218 AA.
XX
AC AAW95664;
XX
DT 08-JUN-1999 (first entry)
XX
DE Mus musculus anti-IgE e26 & e27 variable light chain Fab fragment.
XX
KW Variable light Fab fragment; antibody; anti-IgE; reduction; prevention;
KW histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW eczema; anaphylactic shock; urticaria; IgE.
XX
OS Mus musculus.
XX
PN WO9901556-A2.
XX
PD 14-JAN-1999.
XX
PF 30-JUN-1998; 98WO-US13410.
XX
PR 02-JUL-1997; 97US-0887352.

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:28:52 ; Search time 9.42176 Seconds
(without alignments)
978.986 Million cell updates/sec

Title: US-09-802-077-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGDVRT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1135	100.0	218	2	US-08-887-352B-13
2	1135	100.0	218	3	US-08-466-151-9
3	1135	100.0	218	3	US-09-109-207C-13
4	1135	100.0	218	3	US-09-296-005-13
5	1135	100.0	218	4	US-08-466-163B-9
6	1112	98.0	218	3	US-09-282-505-1
7	1112	98.0	218	3	US-09-054-255-1
8	1112	98.0	218	4	US-09-282-846-1
9	1112	98.0	218	4	US-09-680-145-1
10	1109	97.7	218	2	US-08-887-352B-15
11	1109	97.7	218	2	US-08-887-352B-17
12	1109	97.7	218	2	US-08-887-352B-19
13	1109	97.7	218	2	US-08-887-352B-24
14	1109	97.7	218	3	US-09-109-207C-15
15	1109	97.7	218	3	US-09-109-207C-17
16	1109	97.7	218	3	US-09-109-207C-19
17	1109	97.7	218	3	US-09-109-207C-24
18	1109	97.7	218	3	US-09-296-005-15
19	1109	97.7	218	3	US-09-296-005-17
20	1109	97.7	218	3	US-09-296-005-19
21	1109	97.7	218	3	US-09-296-005-24
22	1108	97.6	218	5	PCT-US96-13152-2
23	1021	90.0	214	2	US-07-934-373C-39
24	1021	90.0	214	3	US-08-437-642B-39
25	1021	90.0	214	5	PCT-US93-07832-39
26	1016	89.5	214	2	US-07-934-373C-40
27	1016	89.5	214	2	US-08-788-800-11

28	1016	89.5	214	3	US-08-437-642B-40	Sequence 40, Appl
29	1016	89.5	214	3	US-09-097-309-2	Sequence 2, Appli
30	1016	89.5	214	3	US-09-097-171A-2	Sequence 2, Appli
31	1016	89.5	214	4	US-09-460-587-2	Sequence 2, Appli
32	1016	89.5	214	5	PCT-US93-07832-40	Sequence 40, Appl
33	1016	89.5	233	2	US-07-934-373C-25	Sequence 25, Appl
34	1016	89.5	233	3	US-08-437-642B-25	Sequence 25, Appl
35	1016	89.5	233	4	US-08-146-206C-25	Sequence 25, Appl
36	1016	89.5	233	5	PCT-US93-07832-25	Sequence 25, Appl
37	1016	89.5	237	3	US-09-097-309-6	Sequence 6, Appli
38	1016	89.5	237	3	US-09-097-171A-10	Sequence 10, Appl
39	1016	89.5	237	3	US-09-422-712B-2	Sequence 2, Appli
40	1016	89.5	237	3	US-09-607-756-2	Sequence 2, Appli
41	1016	89.5	237	4	US-09-460-587-6	Sequence 6, Appli
42	1011.5	89.1	242	3	US-09-027-449-62	Sequence 62, Appl
43	1011.5	89.1	242	3	US-09-026-985-62	Sequence 62, Appl
44	1011.5	89.1	242	4	US-09-121-952A-62	Sequence 62, Appl
45	1011.5	89.1	242	4	US-09-234-340A-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-08-887-352B-13
; Sequence 13, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887.352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-13

Query Match 100.0%; Score 1135; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.le-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DIQLTQSPSSLSASVGDVRTITTCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLES 60	
Db	1	DIQLTQSPSSLSASVGDVRTITTCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLES 60	
Qy	61	GVPSRFSGSGSGTDFTLTITSLQPEDFATYYCQQSHEDPYTFGGTKVEIKRTVAAPSVF 120	
Db	61	GVPSRFSGSGSGTDFTLTITSLQPEDFATYYCQQSHEDPYTFGGTKVEIKRTVAAPSVF 120	

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 2
US-08-466-151-9
; Sequence 9, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-9

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218

Db 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 3
US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218
Db 181 STLTLKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 218

RESULT 4
US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypepti
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:

```
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match      100.0%; Score 1135; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
   |||||||
Db 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
   |||||||

QY 61 GVPSRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||||||
Db 61 GVPSRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||||||

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||

RESULT 5
US-08-466-163B-9
; Sequence 9, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1, light chain
US-08-466-163B-9

Query Match      100.0%; Score 1135; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.1e-86;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
   |||||||
Db 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
   |||||||

QY 61 GVPSRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||||||
Db 61 GVPSRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||||||

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||
```

```
RESULT 6
US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match      98.0%; Score 1112; DB 3; Length 218;
Best Local Similarity 98.2%; Pred. No. 9.2e-85;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
   |||||||
Db 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
   |||||||

QY 61 GVPSRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||||||
Db 61 GVPSRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||||||

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
   |||||||

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
   |||||||

RESULT 7
US-09-054-255-1
; Sequence 1, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1

Query Match      98.0%; Score 1112; DB 3; Length 218;
Best Local Similarity 98.2%; Pred. No. 9.2e-85;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
   |||||||
Db 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLE 60
   |||||||

QY 61 GVPSRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
   |||||||
```

Db 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8
US-09-282-846-1
; Sequence 1, Application US/09282846
; Patent No. 6528624
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R2
; CURRENT APPLICATION NUMBER: US/09/282,846
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6528624
US-09-282-846-1

Query Match 98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 9.2e-85;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGDSYMNNWYQQKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYMNNWYQQKPGKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9
US-09-680-145-1
; Sequence 1, Application US/09680145
; Patent No. 6538124
; GENERAL INFORMATION:
; APPLICANT: Esohe Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/680,145
; CURRENT FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 09/282,505
; PRIOR FILING DATE: 1999-03-13
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6538124
US-09-680-145-1

Query Match 98.0%; Score 1112; DB 4; Length 218;
Best Local Similarity 98.2%; Pred. No. 9.2e-85;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGDSYMNNWYQQKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYMNNWYQQKPGKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10
US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15

Query Match 97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGDSYMNNWYQQKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDYLNWYQQKPGKAPKLLIYAASYLES 60

QY 61 GVPSTRFSGSGGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
Db 61 GVPSTRFSGSGGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 11
US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

Query Match 97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSTRFSGSGGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
Db 61 GVPSTRFSGSGGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 12
US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-19

Query Match 97.7%; Score 1109; DB 2; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.6e-84;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSTRFSGSGGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
Db 61 GVPSTRFSGSGGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
RESULT 13
US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM protein - protein search, using sw model
Run on: August 12, 2003, 16:31:48 ; Search time 23.392 Seconds
(without alignments)
1186.320 Million cell updates/sec

Title: US-09-802-077-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGDVRT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 479057 seqs, 127295195 residues
Total number of hits satisfying chosen parameters: 479057

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	1135	100.0		218	9	US-09-802-077-9	Sequence 9, Appli
2	1135	100.0		218	9	US-09-802-096-9	Sequence 9, Appli
3	1135	100.0		218	9	US-09-920-171-13	Sequence 13, Appl
4	1135	100.0		218	11	US-09-925-179-9	Sequence 9, Appli
5	1120	98.7		218	11	US-09-925-179-67	Sequence 67, Appl
6	1109	97.7		218	9	US-09-920-171-15	Sequence 15, Appl
7	1109	97.7		218	9	US-09-920-171-17	Sequence 17, Appl
8	1109	97.7		218	9	US-09-920-171-19	Sequence 19, Appl
9	1109	97.7		218	9	US-09-920-171-24	Sequence 24, Appl
10	1108	97.6		218	9	US-09-917-410-2	Sequence 2, Appli
11	1100	96.9		238	15	US-10-216-484-127	Sequence 127, App
12	1099	96.8		238	15	US-10-216-484-131	Sequence 131, App
13	1096	96.6		238	15	US-10-216-484-129	Sequence 129, App
14	1036	91.3		214	15	US-10-153-382-19	Sequence 19, Appl
15	1036	91.3		238	15	US-10-216-484-107	Sequence 107, App

16	1031	90.8	238	15	US-10-216-484-50	Sequence 50, Appl
17	1019	89.8	218	15	US-10-171-452A-39	Sequence 39, Appl
18	1019	89.8	218	15	US-10-171-452A-57	Sequence 57, Appl
19	1019	89.8	238	15	US-10-171-452A-38	Sequence 38, Appl
20	1019	89.8	238	15	US-10-171-452A-56	Sequence 56, Appl
21	1018	89.7	238	15	US-10-216-484-52	Sequence 52, Appl
22	1017	89.6	238	15	US-10-216-484-109	Sequence 109, App
23	1016	89.5	214	9	US-09-940-166A-2	Sequence 2, Appli
24	1016	89.5	214	9	US-09-811-384-11	Sequence 11, Appl
25	1016	89.5	237	9	US-09-940-166A-6	Sequence 6, Appli
26	1016	89.5	237	15	US-10-227-694-1	Sequence 1, Appli
27	1016	89.5	238	15	US-10-216-484-54	Sequence 54, Appl
28	1013	89.3	236	10	US-09-859-053-30	Sequence 30, Appl
29	1013	89.3	237	9	US-09-056-160B-100	Sequence 100, App
30	1013	89.3	237	15	US-10-020-786-10	Sequence 10, Appl
31	1013	89.3	491	14	US-10-011-125-2	Sequence 2, Appli
32	1012.5	89.2	241	15	US-10-221-945-1	Sequence 1, Appli
33	1011.5	89.1	242	11	US-09-726-258-62	Sequence 62, Appl
34	1010.5	89.0	242	11	US-09-726-258-51	Sequence 51, Appl
35	1010	89.0	237	15	US-10-020-786-8	Sequence 8, Appli
36	1010	89.0	237	15	US-10-227-694-4	Sequence 4, Appli
37	1009	88.9	218	15	US-10-171-452A-45	Sequence 45, Appl
38	1009	88.9	218	15	US-10-171-452A-51	Sequence 51, Appl
39	1009	88.9	238	15	US-10-171-452A-44	Sequence 44, Appl
40	1009	88.9	238	15	US-10-171-452A-50	Sequence 50, Appl
41	1008	88.8	234	9	US-09-740-002-24	Sequence 24, Appl
42	1007.5	88.8	219	11	US-09-726-258-72	Sequence 72, Appl
43	1007.5	88.8	242	11	US-09-726-258-56	Sequence 56, Appl
44	1007	88.7	214	15	US-10-253-366-1	Sequence 1, Appli
45	1007	88.7	214	15	US-10-316-694-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-802-077-9
; Sequence 9, Application US/09802077
; Patent No. US20010033842A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C2US
; CURRENT APPLICATION NUMBER: US/09/802,077
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae1l, version 1, light chain
US-09-802-077-9

Query Match 100.0%; Score 1135; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASYLES 60

QY 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 2
US-09-802-096-9
; Sequence 9, Application US/09802096
; Patent No. US20010038839A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
; FILE REFERENCE: P0718P2C3US
; CURRENT APPLICATION NUMBER: US/09/802,096
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael, version 1, light chain

US-09-802-096-9
Query Match 100.0%; Score 1135; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11

US-09-920-171-13
Query Match 100.0%; Score 1135; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQQKPGKAPKLLIYAASYLES 60
QY 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Db 61 GVPSRFGSGSGTDFTLTISSLOPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYLS 180
QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4
US-09-925-179-9
; Sequence 9, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mael, version 1, light chain

US-09-925-179-9
Query Match 100.0%; Score 1135; DB 11; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSVDDYDGDSYMWNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDVRTITCRASQSVDDYDGDSYMWNWYQOKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDFLTITSSLPEDFATYYCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
Db 61 GVPSRFSGSGGTDFLTITSSLPEDFATYYCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5
US-09-925-179-67
; Sequence 67, Application US/09925179
; Publication No. US20030044858A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P0718P2C1D1C1US
; CURRENT APPLICATION NUMBER: US/09/925,179
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 08/466,163
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: PCT/US92/06860
; PRIOR FILING DATE: 1992-08-14
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 67
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Full-length light chain sequence corresponding to F(ab)9 of Table
US-09-925-179-67

Query Match 98.7%; Score 1120; DB 11; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.9e-72;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSVDDYDGDSYMWNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSVSGDRATITCRASQSVDDYDGDSYMWNWYQOKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDFLTITSSLPEDFATYYCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
Db 61 GIPSRFSGSGGTDFLTITSSVQPEDFATYYCQSHEDPYTFGGQTKLEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6
US-09-920-171-15

; Sequence 15, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-15

Query Match 97.7%; Score 1109; DB 9; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.2e-71;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSVDDYDGDSYMWNWYQOKPGKAPKLLIYAASYLE 60
Db 1 DIQLTQSPSSLSASVGDVRTITCRASKPVDGEGDSYLNWYQOKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
Db 61 GVPSRFSGSGGTDFLTITSSLPQEDFATYYCQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7
US-09-920-171-17
; Sequence 17, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-920-171-17

Query Match 97.7%; Score 1109; DB 9; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.2e-71;

Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSYMWNWYQKPGKAPKLLIYAASYLES 60
|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLES 60
|||||

QY 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
|||||
Db 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
|||||

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
|||||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
|||||

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||||

RESULT 8
US-09-920-171-19
; Sequence 19, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 19
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-920-171-19

Query Match 97.7%; Score 1109; DB 9; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.2e-71;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSYMWNWYQKPGKAPKLLIYAASYLES 60
|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLES 60
|||||

QY 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
|||||
Db 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
|||||

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
|||||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
|||||

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||||

RESULT 9
US-09-920-171-24
; Sequence 24, Application US/09920171
; Patent No. US20020054878A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.

; APPLICANT: Jardieu, Paula M.
; APPLICANT: Lowe, John
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 24
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Light chain F(ab)'2 sequence derived from MAE11
US-09-920-171-24

Query Match 97.7%; Score 1109; DB 9; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.2e-71;
Matches 213; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSYMWNWYQKPGKAPKLLIYAASYLES 60
|||||
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLES 60
|||||

QY 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
|||||
Db 61 GVPSPRFGSGSGTDFTLTISSLPQEDFATYYCQOSHEDPYTFGGQTKVEIKRTVAAPSVF 120
|||||

QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
|||||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSL 180
|||||

QY 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||||

RESULT 10
US-09-917-410-2
; Sequence 2, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO, Man S.
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII, WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/917,410
FILING DATE: 26-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/578,953
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 95 114 969.9
FILING DATE: 19-Sep-95

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020098183Alman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 218
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-917-410-2

Query Match 97.6%; Score 1108; DB 9; Length 218;
Best Local Similarity 97.2%; Pred. No. 1.4e-71;
Matches 212; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQMTQSPSSLSASVGDVRTITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 60
QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 61 GIPSRFSGSGSGTDFTLTISSLPEDFATYYCQSNEDPWTFFGGTKVEIKRTVAAPSVF 120
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 11
US-10-216-484-127
Sequence 127, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 127
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-127
Query Match 96.9%; Score 1100; DB 15; Length 238;
Best Local Similarity 97.7%; Pred. No. 5.5e-71;
Matches 213; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 21 DIVLTQSPSSLSASVGDVRTITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 80

QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 81 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSNEDPRTFFGGTKVEIKRTVAAPSVF 140
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
QY 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 201 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 12
US-10-216-484-131
Sequence 131, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 131
LENGTH: 238
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Designed light
OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-131
Query Match 96.8%; Score 1099; DB 15; Length 238;
Best Local Similarity 97.2%; Pred. No. 6.5e-71;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIQLTQSPSSLSASVGDVRTITCRASQSDYDGDSDYNNWYQKPGKAPKLLIYAASYLE 60
Db 21 DIVLTQSPSSLSASVGDVRTITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLES 80
QY 61 GVPFRFSGSGSGTDFTLTISSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
Db 81 GIPSRFSGSGSGTDFTLTISSLPEDFATYYCQSNEDPRTFFGGTKVEIKRTVAAPSVF 140
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Db 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
QY 181 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 218
Db 201 STLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 13
US-10-216-484-129
Sequence 129, Application US/10216484
Publication No. US20030103976A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:26:07 ; Search time 9.74665 seconds
(without alignments)
2150.973 Million cell updates/sec

Title: US-09-802-077-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGDVRT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	942.5	83.0	215	2 JE0242	Ig kappa chain NIG
2	917.5	80.8	215	2 JE0244	Ig kappa chain NIG
3	892.5	78.6	215	2 JE0243	Ig kappa chain NIG
4	883	77.8	216	2 JE0241	Ig kappa chain Am3
5	875.5	77.1	215	2 A23746	Ig kappa chain V-I
6	759	66.9	240	2 S06084	Ig kappa chain pre
7	739	65.1	218	2 S68241	Ig kappa chain V r
8	737	64.9	218	2 JC5810	monoclonal antibod
9	727	64.1	230	2 S33161	Ig kappa chain - S
10	723	63.7	220	2 A31790	Ig kappa chain V r
11	718	63.3	234	2 S14237	Ig kappa chain pre
12	716	63.1	234	2 S01320	Ig kappa chain pre
13	712	62.7	210	2 A56169	Ig kappa chain V r
14	699	61.6	214	2 S68212	Ig kappa chain (Ma
15	698.5	61.5	219	2 S38865	Ig kappa chain - m
16	694.5	61.2	217	2 S42772	Ig kappa chain - m
17	693.5	61.1	225	2 S37484	Ig kappa chain - m
18	692.5	61.0	219	2 PC4203	Ig kappa chain (mo
19	689.5	60.7	219	2 S52028	Ig kappa chain - m
20	687.5	60.6	235	2 S25058	Ig kappa chain - m
21	683.5	60.2	219	2 S16112	Ig kappa chain V r
22	670.5	59.1	225	2 JL0029	Ig kappa chain pre
23	608	53.6	135	2 S52059	JC-kappa chain pre
24	596	52.5	178	2 PT0219	Ig kappa chain V-C
25	563.5	49.6	229	2 A20969	Ig kappa chain pre
26	548	48.3	106	1 K3HU	Ig kappa chain C r
27	535.5	47.2	197	2 S29593	Ig kappa chain (WM
28	534.5	47.1	238	2 A49633	Ig lambda-like cha
29	513	45.2	99	2 A37927	Ig kappa chain C r

30	507	44.7	99	2 S26653	Ig kappa chain C r
31	505	44.5	127	2 S40367	Ig kappa chain V-J
32	498	43.9	233	2 S29577	Ig light chain - r
33	494	43.5	123	2 S40331	Ig kappa chain - h
34	493	43.4	108	2 B49047	Ig kappa chain V r
35	482	42.5	109	2 S31998	Ig kappa chain - h
36	481	42.4	141	2 A49134	Ig kappa chain V-I
37	478	42.1	108	2 S44122	Ig kappa chain V r
38	477	42.0	144	2 PL0106	Ig kappa chain pre
39	476	41.9	108	2 S47182	Ig kappa chain - h
40	475	41.9	139	2 S40365	Ig kappa chain - h
41	472	41.6	120	2 S46370	Ig kappa chain V-J
42	471	41.5	108	1 K1HUHU	Ig kappa chain V-I
43	471	41.5	109	2 S31981	Ig kappa chain - h
44	470	41.4	132	2 S40334	Ig kappa chain - h
45	469.5	41.4	125	2 S40315	Ig kappa chain - h

ALIGNMENTS

RESULT 1
JE0242
Ig kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis:
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 83.0%; Score 942.5; DB 2; Length 215;
Best Local Similarity 83.5%; Pred. No. 1.3e-55;
Matches 182; Conservative 13; Mismatches 20; Indels 3; Gaps 1;

QY	1	DIQLTQSPSSLSASVGDVRTITCRASQSVDDYDGDSDYMNWYQKPGKAPKLLIYAASYLES 60	
Db	1	EIVLTQSPGTLSPGERATLSCRASQSV---SNNYLAWYQKPGQAPSLLIYDASSRAT 57	
QY	61	GVPSRFSGSGGTDFLTITSSLPEDFATYICQOSHEDPYTFQGQTKVEIKRTVAAPSVF 120	
Db	58	GIPDRFSGSGGTDFILITISGLEPDEFAVYICQYDRPPWTFQGQTKVEIKRTVAAPSVF 117	
QY	121	IFPPSDEQLKSGFASVVCVLLNFPYBREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180	
Db	118	IFPPSDEQLKSGFASVVCVLLNFPYBREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 177	
QY	181	STLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC 218	
Db	178	STLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC 215	

RESULT 2
JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H. submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:22:22 ; Search time 5.84799 Seconds
(without alignments)
1753.051 Million cell updates/sec

Title: US-09-802-077-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLASVGDVRT.....EVTHQGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	548	48.3	106	1	KAC_HUMAN	P01834 homo sapien
2	471	41.5	108	1	KV1H_HUMAN	P01600 homo sapien
3	467	41.1	111	1	KV3M_MOUSE	P01665 mus musculus
4	463	40.8	108	1	KV1E_HUMAN	P01597 homo sapien
5	462	40.7	111	1	KV3Q_MOUSE	P01667 mus musculus
6	460	40.5	111	1	KV3N_MOUSE	P01666 mus musculus
7	460	40.5	129	1	KV1W_HUMAN	P04431 homo sapien
8	459	40.4	111	1	KV3Q_MOUSE	P01669 mus musculus
9	455	40.1	111	1	KV3L_MOUSE	P01664 mus musculus
10	454	40.0	108	1	KV1V_HUMAN	P04430 homo sapien
11	452	39.8	108	1	KV1N_HUMAN	P01606 homo sapien
12	448	39.5	108	1	KV1B_HUMAN	P01594 homo sapien
13	448	39.5	108	1	KV1M_HUMAN	P01605 homo sapien
14	446.5	39.3	110	1	KV3P_MOUSE	P01668 mus musculus
15	444	39.1	108	1	KV1K_HUMAN	P01603 homo sapien
16	444	39.1	108	1	KV1S_HUMAN	P01611 homo sapien
17	443	39.0	108	1	KV1F_HUMAN	P01598 homo sapien
18	443	39.0	108	1	KV1Q_HUMAN	P01607 homo sapien
19	442	38.9	108	1	KV1G_HUMAN	P01599 homo sapien
20	441	38.9	108	1	KV1Y_HUMAN	P80362 homo sapien
21	439	38.7	108	1	KV1R_HUMAN	P01610 homo sapien
22	438	38.6	108	1	KV1P_HUMAN	P01608 homo sapien
23	437	38.5	108	1	KV1L_HUMAN	P01604 homo sapien
24	431	38.0	108	1	KV1A_HUMAN	P01593 homo sapien
25	430.5	37.9	109	1	KV1T_HUMAN	P01612 homo sapien
26	429.5	37.8	107	1	KV1D_HUMAN	P01596 homo sapien
27	429	37.8	111	1	KV3H_MOUSE	P01660 mus musculus
28	425	37.4	108	1	KV1Q_HUMAN	P01609 homo sapien
29	423	37.3	108	1	KV1C_HUMAN	P01595 homo sapien
30	420	37.0	111	1	KV3J_MOUSE	P01662 mus musculus
31	419	36.9	129	1	KV1X_HUMAN	P04432 homo sapien
32	415	36.6	131	1	KV3I_MOUSE	P01661 mus musculus
33	411	36.2	111	1	KV3K_MOUSE	P01663 mus musculus

ALIGNMENTS

RESULT 1				
KAC_HUMAN				
ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ig kappa chain C region.			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,			
RA	Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Franek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press,			
RL	New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa type).";			

P01625 homo sapien
P06314 homo sapien
P01670 mus musculus
P01671 mus musculus
P01613 homo sapien
P01659 mus musculus
P01658 mus musculus
P01602 homo sapien
P18135 homo sapien
P18136 homo sapien
P01673 mus musculus
P01620 homo sapien

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
RN [9]
RP SEQUENCE OF 1-33; 38-41 AND 62-80.
RC TISSUE=Abdominal adipose tissue;
RX PubMed=9588180;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
RT subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00241; AAA58989.1; -;
DR EMBL; V00557; CAA23823.1; -;
DR PIR; B90562; K3HU.
DR PDB; 1D5B; 09-FEB-00.
DR PDB; 1D51; 09-FEB-00.
DR PDB; 1D6V; 04-OCT-00.
DR PDB; 1HEZ; 10-AUG-01.
DR PDB; 1HKL; 12-MAR-97.
DR PDB; 1I72; 08-AUG-01.
DR PDB; 1MIM; 15-MAY-97.
DR Genew; HGNC:5716; IGKC.
DR MIM; 147200; -;
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT VARIANT 83 83 V -> L (IN INV(1,2) MARKER).
FT CONFLICT 14 14 /FTID=VAR_003897.
FT CONFLICT 57 57 D -> N (IN REF. 7 AND 8).
FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;

Query Match 48.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.9e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 172

Db .
1 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 173 KDSFYSLSSTLTLSKADYKHKYVACEVTHOGLSSPVTKSFNRGEC 218
|||||
Db 61 KDSFYSLSSTLTLSKADYKHKYVACEVTHOGLSSPVTKSFNRGEC 106

RESULT 2
KV1H_HUMAN
ID KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868; K1HUHU.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 41.5%; Score 471; DB 1; Length 108;
Best Local Similarity 82.1%; Pred. No. 1.5e-32;
Matches 92; Conservative 10; Mismatches 6; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLASVGDRTVITCRASQSVDYDGDSDYNNWYQKPKAPKLLIYAASYLES 60
|||:|||||
Db 1 DIQMTQSPSSLASVGDRTVITCRASQSI---SSYLSWYQKPKAPQVLIYAASSLPS 56

QY 61 GVPSRFSGSGGTDFLTITISLQPEDFATYYCQSHEDPYTFGGTKVEIKR 112
|||||
Db 57 GVPSRFSGSGGTDFLTITISLQPEDFATYYCQNYITPTSFGGTRVEIKR 108

RESULT 3
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)


```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE..
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01872; K1HUOU.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;

Query Match 39.8%; Score 452; DB 1; Length 108;
Best Local Similarity 70.5%; Pred. No. 5.6e-31;
Matches 79; Conservative 21; Mismatches 8; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGSYMNWYQQKPGKAPKLLIYAASYLES 60
Db 1 DIQMTZSPSSLSASVGBRVITITCRASZTI----SSYLBWYZZKPGKAPBLLIYAASBLHS 56

QY 61 GVPSPRFGSGSGTDFLTITSSLPQEDFATYYCQOSHEDPYTFGQGTKVEIKR 112
Db 57 GVPSPRFGSGSGTBFITITSSLPZPBFBATYYCZSSYSTTFGZGTRLZIKR 108

RESULT 12
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=77022433; PubMed=1234024;
```

```
RA Fehlgammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the
RT Bence-Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC REGION OF THE KAPPA CHAIN REI.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A91653; K1HUAU.
DR PDB; 1JUV5; 30-JAN-02.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding activity; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11939 MW; E8011187EE6F6B9 CRC64;

Query Match 39.5%; Score 448; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 1.2e-30;
Matches 89; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDRTVITCRASQSDVDYDGSYMNWYQQKPGKAPKLLIYAASYLES 60
Db 1 DIQMTQSPSSLSASVGDRTVITCQASQDI----SDYLNWYQQKPGKAPKLLIYDASNLES 56

QY 61 GVPSPRFGSGSGTDFLTITSSLPQEDFATYYCQOSHEDPYTFGQGTKVEIKR 112
Db 57 GVPSPRFGSGSGAHFTTITSSLPQEDATYYCQDYDLPWTFGQGTKVEIKR 108

RESULT 13
KV1M_HUMAN
ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; K1HULY.
DR HSSP; P01607; IREI.
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2003, 16:24:12 ; Search time 21.7675 Seconds
(without alignments)
2584.378 Million cell updates/sec

Title: US-09-802-077-9
Perfect score: 1135
Sequence: 1 DIQLTQSPSSLSASVGDRTV.....EVTHOGLSSPVTKSFNRGEC 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10
                  Listing first 45

```

- ```
SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result<br>No. | Score | Query |   | Length | DB | ID     | Description        |
|---------------|-------|-------|---|--------|----|--------|--------------------|
|               |       | Match | % |        |    |        |                    |
| 1             | 926   | 81.6  |   | 234    | 4  | Q8NEK1 | Q8nek1 homo sapien |
| 2             | 892.5 | 78.6  |   | 239    | 4  | Q8NEK0 | Q8nek0 homo sapien |
| 3             | 891.5 | 78.5  |   | 239    | 4  | Q8TCD0 | Q8tcd0 homo sapien |
| 4             | 738   | 65.0  |   | 234    | 11 | Q8R062 | Q8r062 mus musculu |
| 5             | 733   | 64.6  |   | 234    | 11 | Q91WF8 | Q91wf8 mus musculu |
| 6             | 732   | 64.5  |   | 233    | 11 | Q91WS9 | Q91ws9 mus musculu |
| 7             | 731   | 64.4  |   | 214    | 11 | Q9R1A5 | Q9rla5 mus musculu |
| 8             | 730   | 64.3  |   | 234    | 11 | Q8VCP0 | Q8vcp0 mus musculu |
| 9             | 703.5 | 62.0  |   | 238    | 11 | Q99M37 | Q99m37 mus musculu |
| 10            | 693.5 | 61.1  |   | 238    | 11 | Q8VCI6 | Q8vci6 mus musculu |
| 11            | 693.5 | 61.1  |   | 239    | 11 | Q8VC55 | Q8vc55 mus musculu |
| 12            | 684.5 | 60.3  |   | 235    | 11 | Q91W12 | Q91w12 mus musculu |
| 13            | 679.5 | 59.9  |   | 239    | 11 | Q8K0F8 | Q8k0f8 mus musculu |
| 14            | 662   | 58.3  |   | 234    | 11 | Q8R028 | Q8r028 mus musculu |
| 15            | 487   | 42.9  |   | 108    | 4  | Q9UL77 | Q9ul77 homo sapien |
| 16            | 475.5 | 41.9  |   | 107    | 4  | Q96SA9 | Q96sa9 homo sapien |

|    |       |      |     |    |        |        |              |
|----|-------|------|-----|----|--------|--------|--------------|
| 17 | 459   | 40.4 | 116 | 4  | Q96PF6 | Q96pf6 | homo sapien  |
| 18 | 450.5 | 39.7 | 107 | 4  | Q9UL81 | Q9ul81 | homo sapien  |
| 19 | 446   | 39.3 | 108 | 4  | Q9UL70 | Q9ul70 | homo sapien  |
| 20 | 445   | 39.2 | 236 | 4  | Q8NEJ1 | Q8nej1 | homo sapien  |
| 21 | 440.5 | 38.8 | 237 | 4  | Q8WUK4 | Q8wuk4 | homo sapien  |
| 22 | 439.5 | 38.7 | 233 | 4  | Q8TBC9 | Q8tbc9 | homo sapien  |
| 23 | 439.5 | 38.7 | 237 | 4  | Q8WTU6 | Q8wtu6 | homo sapien  |
| 24 | 435   | 38.3 | 108 | 4  | Q9UL79 | Q9ul79 | homo sapien  |
| 25 | 422   | 37.2 | 234 | 4  | Q8N355 | Q8n355 | homo sapien  |
| 26 | 413.5 | 36.4 | 233 | 4  | Q8N5F4 | Q8n5f4 | homo sapien  |
| 27 | 413   | 36.4 | 111 | 11 | Q920E9 | Q920e9 | mus musculus |
| 28 | 403.5 | 35.6 | 236 | 4  | Q96E61 | Q96e61 | homo sapien  |
| 29 | 397.5 | 35.0 | 235 | 11 | Q99M11 | Q99m11 | mus musculus |
| 30 | 395   | 34.8 | 240 | 4  | Q8WUK3 | Q8wuk3 | homo sapien  |
| 31 | 391   | 34.4 | 298 | 11 | Q9QYF0 | Q9qyf0 | mus musculus |
| 32 | 389.5 | 34.3 | 112 | 11 | Q8K1F3 | Q8k1f3 | mus musculus |
| 33 | 388.5 | 34.2 | 114 | 11 | Q8K1F1 | Q8k1f1 | mus musculus |
| 34 | 387.5 | 34.1 | 109 | 4  | Q9UL78 | Q9ul78 | homo sapien  |
| 35 | 380   | 33.5 | 109 | 11 | Q920E6 | Q920e6 | mus musculus |
| 36 | 379.5 | 33.4 | 112 | 11 | Q8K1F2 | Q8k1f2 | mus musculus |
| 37 | 376   | 33.1 | 108 | 4  | Q9UL83 | Q9ul83 | homo sapien  |
| 38 | 372   | 32.8 | 108 | 11 | Q8V1J0 | Q8vij0 | mus musculus |
| 39 | 369.5 | 32.6 | 109 | 4  | Q9UL86 | Q9ul86 | homo sapien  |
| 40 | 367.5 | 32.4 | 134 | 11 | Q8VDD0 | Q8vdd0 | mus musculus |
| 41 | 366   | 32.2 | 103 | 11 | Q9JL80 | Q9jl80 | mus musculus |
| 42 | 365.5 | 32.2 | 233 | 4  | Q96I69 | Q96i69 | homo sapien  |
| 43 | 359.5 | 31.7 | 109 | 4  | Q9UL85 | Q9ul85 | homo sapien  |
| 44 | 353   | 31.1 | 107 | 11 | Q9JL84 | Q9jl84 | mus musculus |
| 45 | 351.5 | 31.0 | 112 | 11 | Q8K1F0 | Q8k1f0 | mus musculus |

## ALIGNMENTS

|        |                                                          |
|--------|----------------------------------------------------------|
| RESULT | 1                                                        |
| Q8NEK1 | PRELIMINARY; PRT; 234 AA.                                |
| ID     | Q8NEK1                                                   |
| AC     | Q8NEK1;                                                  |
| DT     | 01-OCT-2002 (TREMBLrel. 22, Created)                     |
| DT     | 01-OCT-2002 (TREMBLrel. 22, Last sequence update)        |
| DT     | 01-MAR-2003 (TREMBLrel. 23, Last annotation update)      |
| DE     | Hypothetical protein.                                    |
| OS     | Homo sapiens (Human).                                    |
| OC     | Eukaryota; Metazoa; Chordata; Vertebrata; Eute-          |
| OC     | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom |
| OX     | NCBI_TaxID=9606;                                         |
| RN     | [1]                                                      |
| RP     | SEQUENCE FROM N.A.                                       |
| RC     | TISSUE=Lung;                                             |
| RA     | Strausberg R.;                                           |
| RL     | Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. |
| DR     | EMBL; BC030813; AAH30813.1; -                            |
| DR     | InterPro; IPR007110; Ig-like.                            |
| DR     | InterPro; IPR003597; Ig_cl.                              |
| DR     | InterPro; IPR003006; Ig_MHC.                             |
| DR     | InterPro; IPR003596; Ig_v.                               |
| DR     | Pfam; PF00047; ig; 2.                                    |
| DR     | SMART; SM00407; IGcl; 1.                                 |
| DR     | SMART; SM00406; IgV; 1.                                  |
| DR     | PROSITE; PS50835; IG_LIKE; 2.                            |
| DR     | PROSITE; PS00290; IG_MHC; 1.                             |
| KW     | Hypothetical protein.                                    |
| SQ     | SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;       |

|    |                                                                  |        |            |          |                        |
|----|------------------------------------------------------------------|--------|------------|----------|------------------------|
|    | Query Match                                                      | 81.6%; | Score 926; | DB 4;    | Length 234;            |
|    | Best Local Similarity                                            | 82.1%; | Pred. NO.  | 4.3e-77; |                        |
|    | Matches 179; Conservative                                        | 19;    | Mismatches | 16;      | Indels      Gaps    1; |
| Qy | 1 DIQLTQSPSLSSASVGDRTVTITCRASQSVDYDGDYSVMNMYQQKPGKAPKLLIYAASYLES | 60     | :          | :     :  | :       :              |
| Dδ | 21 EIVMTQPATLSVPGERATLSCRASQSV---TSNLAWYQQTTPGQSPRLVIYGASSRAS    | 76     | :          | :     :  | :       :              |
| Qv | 61 GVPSRFSGGGSDFTLTIISSLOPEDFATYYCOOSHEDPPYTFGOGTKEIKRTRYAAPSFVF | 120    | :          | :     :  | :       :              |











